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# ASSISTANT COMMISSIONER FOR PATENTS WASHINGTON, D.C. 20231

Art Unit\_

Sir:

This is a request for filing a

- (X) Continuation application,
- ( ) Divisional application,

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under 37 CFR §1.60, of pending prior application Serial No. 08/788,882 filed on January

21, 1997 of Needleman et al. for AN IMMUNOLOGICAL PROCESS AND CONSTRUCTS FOR

## INCREASING THE HDL CHOLESTEROL CONCENTRATION

- 2. (X) The filing fee is calculated below:

# CLAIMS AS FILED IN THE PRIOR APPLICATION, LESS ANY CLAIMS CANCELLED BY AMENDMENT BELOW

For	No. Filed	No. Extra	Rate	Fee
Basic Fee				\$ 760.00
Independent Claims	1 - 3 =		x \$82.00 =	\$0
Total Claims	7 - 20 =		x \$18.00 =	\$0
		Total Filing Fee		\$ 760.00
Statement of Status as Small Entity Reducing Filing Fee by Half to				\$00

3. ( )	Verified statements (Declarations) claiming small entity status were filed in the prior application and small entity status for this application is proper and desired.
4. (X)	A check in the amount of \$_760.00 is enclosed.
5. (X)	The Commissioner is hereby authorized to charge any additional fees which may be required for this application under 37 CFR §§1.16-1.17, or credit any overpayment, to Deposit Account No. 23-0920. A duplicate copy of this sheet is enclosed.
6. (X)	Cancel in this application original claims 1-10, and 18-43 of the prior application before calculating the filing fee.
7. (X)	Amend the specification by inserting before the first line the sentence: — This is a (X) continuation, () division, of application Serial No. <u>08/788,882</u> , filed <u>January 21, 1997</u> .—
8. ( )	Transfer the drawings from the prior application to this application and abandon said prior application as of the filing date accorded this application. A duplicate copy of this sheet is enclosed for filing in the prior application file. (May be used only if signed by person authorized by '1.138 and before payment of base issue fee.)
8a. ( )	New formal drawings are enclosed.
9. ( X)	Other: STATEMENT UNDER 37 CFR § 1.821(f) and computer readable disk with prior sequence listing from parent application.
10. ( )	Priority of application Serial No filed on in is claimed under 35 USC §119.
11. (X)	The prior application is assigned of record to Monsanto Company.
12. ( X)	The power of attorney in the prior application is to:
	Edward P. Gamson Registration No. 29,381 WELSH & KATZ, LTD. 120 South Riverside Plaza 22nd Floor Chicago, Illinois 60606 and other members of the firm.

- (a) (X)The power appears in the original papers in the prior application.
- (b) ( ) Since the power does not appear in the original papers, a copy of the power in the prior application is enclosed.
- (c) (X) Address all future communications to:

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(May be completed only by applicant, or the attorney or

agent of record.)

- (d) (X) The executed Power of Attorney document filed in the prior application.
- (e) ( ) The executed Verified Statements claiming small entity, filed in the prior application.

August 31, 1999

Edward P. Gamson

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#### Description

## Technical Field

The present invention relates to a process for for raising the HDL cholesterol level in mammalian blood, and more particularly to an immunological process for ameliorating dyslipoproteinemias characterized by low HDL/LDL cholesterol ratios as well as specific immunogenic constructs for use in that process.

### 15 Background of the Invention

Cholesteryl ester transfer protein (CETP) is an acidic plasma glycoprotein that plays a critical role in establishing high density lipoprotein (HDL), low density lipoprotein (LDL), and very low density lipoprotein (VLDL) cholesterol blood plasma levels and lipid composition in plasma [L. Lagrost, Biochem. Biophys. Acta., 1215:209-236 (1994)]. Several studies, some of which are discussed below, have demonstrated that CETP mediates the transfer of cholesterol esters (CE) from HDL particles to LDL and VLDL particles, as well as mediating the transfer of triglycerides (TG) from LDL and VLDL to HDL particles. This reciprocal exchange of CE and TG is the primary means of providing CE to LDL and VLDL particles in many mammalian species. CETP thus mediates the balanced exchange of cholesteryl esters (CE) and triglycerides (TG) between proatherogenic (LDL and VLDL) and anti-atherogenic (HDL) lipoprotein fractions.

Mammalian species whose blood plasma contains CETP such as humans and other primates, rabbits, and hamsters suffer atherosclerosis and heart disease when

exposed to diets rich in cholesterol. Other animal species such as mice, rats and dogs lack plasma CETP (measured as transfer activity) and are not susceptible to dietary cholesterol-induced atherosclerosis.

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That CETP contributes to the pathogenesis of atherosclerosis in humans has been strongly supported by transgenic mouse studies [G. Melchior et al., Trends in Card. Med, 5:83-87 (1995)]. For example, transgenic mice having a mini gene of cynomolgus monkey CETP cDNA plus the proximal region of the CETP promoter show dietary cholesterol regulation of CETP levels similar to those seen in humans, hamsters and monkeys. Those transgenic mice expressing high levels of the monkey CETP (levels comparable to human dyslipidemias) exhibit: increased LDL+VLDL cholesterol and apo-B and, decreased HDL cholesterol, LDL-receptor and HMG-CoA reductase mRNA. Atheroma could be induced by high fat diet in transgenic mice with the cynomolgus monkey CETP transgene.

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The CETP amino acid residue and nucleotide sequences of mammalian species have been characterized. For example, the human CETP DNA sequence of SEQ ID NO:1 has been determined [ D. Drayna et al., Nature, 327:632-634 (1987)]. The rabbit CETP DNA sequence of SEQ ID NO:27 has also been characterized [M. Nagashima et al., J. Lipid Res., 29:1643-1469 (1988)], as has the cynomolgus monkey CETP sequence [M. E. Pape et al., Atherosclerosis and Thrombosis, 11:1759-1771 (1991)]. The human CETP protein is 476 amino acid residues long, whereas the rabbit CETP protein is 496 amino acid residues long, and the cynomolgus monkey sequence contains 476 residues.

CETP may be a key factor for the global regulation of atherogenicity of plasma lipoproteins in patients with atherosclerosis or coronary artery disease

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(CAD). CAD is the number one cause of morbidity and mortality in western society. Patients at increased risk for developing coronary artery disease typically exhibit an enhanced level of CETP activity. It has also been reported that CETP has higher affinity for oxidized LDL than native LDL molecules [L. Lagrost, Biochem. Biophys. Acta., 1215:209-236 (1994)]. High levels of LDL cholesterol (>180 mg/dl) [J. Am. Med. Assoc., 269:3015-3023 (1993) and A. L. Gould et al., Circulation, 91:2274-2282 (1995)]; and low levels of HDL

Circulation, 91:2274-2282 (1995)]; and low levels of HDI cholesterol (<35 mg/dl) [G. Assman et al., Excerpta Medica, 46-59 (1989) and V. Manninen et al., Circulation, 85:37-45 (1992)] have been reported to be important contributors to the development of atherosclerosis.

Individuals who possess genetic deficiencies of the CETP protein have elevated HDL cholesterol levels. Heterozygotes have HDL levels 15-20 percent above non-affected controls. It has been suggested that there is a 2-3 percent decrease in coronary heart disease (CHD) risk for each 1 mg/dl increase in HDL cholesterol after correction for other risk factors [ D. J. Grodon et al., Nature, 79:8-15, (1989)].

In an experimental model of CETP deficiency in hamsters, it has been shown that passive transfer of mouse anti-human CETP monoclonal antibodies (1C4) inhibited hamster plasma CETP CE transfer by 70-80 percent at all times up to 24 hours following injection of 500  $\mu$ g of 1C4 (approximately 3.7 mg/kg body weight). That inhibition of hamster CETP-mediated transfer in vivo increased hamster HDL cholesterol by 33 percent, increased HDL-CE by 31 percent and decreased HDL-TG by 42 percent. These results indicate an example of mammalian (hamster) CETP-mediated CE-TG exchange being disrupted by xenogeneic anti-human CETP monoclonal

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antibodies, and further demonstrate the use of hamsters as pre-clinical model for testing CETP inhibition [B. J. Gaynor et al., Atherosclerosis, 110(1):101-109 (1994)].

In another study reported by G. W. Melchior et al., J. Biol. Chem., 270(36):21068-74 (1995) cynomolgus monkey CETP was shown to have two neutral lipid binding sites. A monoclonal antibody to purified cynomolgus monkey CETP identified as CMTP-2 was capable of severely inhibiting triglyceride (TG) transfer, but had a variable effect on cholesteryl ester (CE) transfer.

Thus, when the monoclonal antibody was administered sub-cutaneously to cynomolgus monkeys at a dose that inhibited TG transfer in the plasma by more than 90 percent, there was no detectable effect on the high density lipoprotein cholesterol level, but the HDL-TG levels decreased from 13 to 1 mol/mol of HDL. A Fab antibody fragment had no effect on CE transfer, but completely blocked TG transfer. Another type of inhibitor, 6-chloromercuric cholesterol, severely inhibited CE transfer with minimal inhibition of TG transfer. When both the inhibitory monoclonal antibody and the 6-chloromercuric cholesterol were added to the assay, both CE and TG transfer were inhibited, indicating that the inhibitors did not compete for the same binding site on CETP. This study indicated that in vivo administration of xenogeneic monoclonal antibodies uncoupled CE and TG transfer.

The inhibitory effects of antisense RNA on expression of CETP protein were reported using vaccinia virus as an expression system. [M. H. Lee et al., J. Biochem. Mol. Biol., 28(3):243-248 (1995)]. The cDNA from CETP was inserted into a transfer vector (pSC11) in sense and antisense orientations and then used to construct recombinant vaccinia viruses. Decreased

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expression of the exogenous CETP cDNA in mouse cells was clearly evident in the Northern and Western blot analyses as the dose of anti-sense expression increased. Also, in the CETP assay, the CETP activity was decreased compared to the activity obtained from the cell extracts infected with sense constructs only.

More recently, Sugano et al., J. Biol. Chem., 271(32):19080-19083 (1996) reported upon the in vivo effects of antisense CETP RNA administration to rabbits. In that report, a decrease in total cholesterol and CETP activity levels were found 24, 48 and 96 hours following antisense CETP administration, as was an increase in plasma HDL cholesterol at 48 hours.

Other methods of inhibition of CETP-mediated transfer are described in the literature. For example, data from Parke-Davis company has shown that infusion of 10 to 20 mpk of the small molecule compound referred to as PD 140195 into rabbits inhibited CETP activity within 30 minutes (measured in an ex vivo assay) [C. Bisgaier et al., Lipids, 811-818 (1994)]. Schering-Plough Company has published on the isolation of Wiedendiol-A and -B from a marine sponge and has shown that this class of compounds to be low  $\mu$ M inhibitors of CETP-mediated CE transfer in vitro [S. Coval et al., Bioorganic & Med. Claim. Lett., 5:605-619 (1995)].

Currently, nicotinic acid and the fibrate drugs are the only small molecule drug therapies that cause significant rises in HDL cholesterol. These drugs are poorly tolerated and must be taken daily.

Therapeutic doses of these drugs lead to 15-20 percent

Therapeutic doses of these drugs lead to 15-20 percent increases in HDL cholesterol.

Three mouse monoclonal antibodies to human CETP that recognize a similar epitope on CETP, caused parallel and complete *in vitro* immunotitration of human plasma CE and triglyceride transfer activities, but only

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partial inhibition of phospholipid transfer activity [C. B. Hesler et al., *J. Biol. Chem.*, 263(11):5020-5023 (1988)]. Those three monoclonals were originally designated 5C7, 2H4 and 7E1, but in more recent publications of the authors, those monoclonals are referred to as TP2, TP1 and TP3, respectively.

Monoclonal antibody TP2 is directed against an epitope within the last 26 amino acids of CETP (SEQ ID NO:29) [T.L. Swenson et al., J. Biol. Chem., 264:14318-14326 (1989)], and more particularly to an epitope between about positions 465 and 475 of SEQ ID NO:28 [Tall, J. Lipid Res., 34:1255-1274 (1993)]. That monoclonal has been shown to block CETP-mediated lipid transfer by limiting access to lipid-binding sites in the carboxy-terminus of CETP.

In an in vivo study using the xenogeneic mouse monoclonal antibodies (TP1) to CETP, rabbits were intravenously injected with TP1, or irrelevant monoclonal antibodies or saline (control), resulting in an initial 70 percent inhibition of CETP-mediated CE transfer activity. Inhibition was reduced to 45 percent after 48 hours for the TP1-injected animals. increased in TP1-treated animals and reached levels that doubled over initial and control values at 48 hours. HDL-TG fell reciprocally, but HDL protein did not change, suggesting a CE for TG exchange. VLDL CE-TG ratio also decreased. CETP inhibition delayed the initial clearance of radioactively-tagged HDL, suggesting that CETP plays a quantitative role in HDL-CE catabolism in the rabbit, promoting the exchange of TG for CE, and the clearance of CE from plasma [M. E. Whitlock et al., J. Clin. Invest., 84:129-137 (1989)].

In further animal studies with hamsters, a single sub-cutaneous injection of TP2 monoclonal antibodies in another illustration of passive

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administration of xenogeneic antibodies decreased CETP-mediated activity by 58 percent, lowered LDL+VLDL cholesterol 32 percent and raised HDL cholesterol 24 percent [G. Evans et al., J. Lipid Res., 35:1634-1645 (1994) and S. Zuckerman et al., Lipids, 30:307-311 (1995)]. The effect of the TP2 monoclonal antibodies on CETP-mediated CE transfer inhibition was evident within 24 hours after injection and was maximized by 4 days. Lipoproteins returned to control levels 14 days after TP2 administration. The shift in the ratio of VLDL+LDL cholesterol to HDL cholesterol levels due to TP2 monoclonal antibody administration was more significant in hypercholesterolemic hamsters.

TP2 also has a higher efficacy in hamsters fed with a western diet enriched in cholesterol. CETP-mediated activity was reportedly increased in these animals 2-fold over chow-fed hamsters.

The preparation of recombinant CETP molecules has been reported by several research groups. For example, in a study reported recently, glutathione S-transferase-human CETP fusion protein (86 kDa) was expressed using vaccinia viral transfer vectors transfected into CV-1 monkey kidney cells. Using a Western blot assay, the fusion protein was identified by polyclonal antibodies against the carboxy-terminal active region of CETP fused with GST. After cleavage of the GST portion of the fusion protein, the purified CETP showed biological activity in a CETP in vitro assay [W. H. Yoon et al., Mol. Cells, 5(2):107-113 (1995)] and M. K. Jang et al., J. Biochem. Mol. Biol., 28(3):216-220 (1995)].

It has also been reported that specific rabbit polyclonal antibodies were produced by immunization with a GST-CETP fusion protein. A full-length CETP cDNA clone isolated from a human heart  $\lambda gt11$  library was used

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to provide the C-terminal 94 bp of CETP after a full length CETP molecule expressed in E. coli was found to be insoluble. The lambda gt11 cDNA library was subcloned into pGEX plasmid and a GST-CETP fusion protein was expressed in E. coli. The CETP-GST fusion protein was purified by glutathione-Sepharose-4B affinity chromatography and used as an antigen for the production of rabbit polyclonal antibodies. antibodies showed good titers, not only against the GST-CETP fusion protein, but also against a mixture of synthetic peptides corresponding in sequence to two 16mers from the carboxy-terminal region of human CETP. The antibodies were said to be useful as an immunological tool for a CETP assay [N.W. Jeong et al., Mol. Cells, 4(4):529-533 (1994)].

To date there are no published reports on the long-term inhibition of CETP-mediated CE transfer. Passive immunization with the use of xenogeneic antibodies can only be utilized for a short-term period of time because host animals develop antibodies to the xenogeneic immunoglobulin. The invention described hereinafter provides an autogeneic immunological means for the long-term lessening of transfer of cholesteryl esters from HDL particles in mammals whose blood contains CETP. This permits the long-term elevation of anti-atherogenic HDL cholesterol concentrations.

## Brief Summary of the Invention

The present invention contemplates an autogeneic immunological process for lessening the transfer of cholesteryl esters from HDL particles and for increasing the HDL cholesterol concentration of a mammal whose blood also contains CETP. A contemplated process is useful in treating human pro-atherogenic dyslipoproteinemias characterized by low HDL/LDL

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cholesterol ratios. Also contemplated here are immunogens utilized in that process, as well as isolated and purified DNA that encodes some of those immunogens and expression systems for that DNA.

One contemplated process comprises the steps of:

(a) immunizing the mammal to be treated with an inoculum containing a CETP immunogen that is dissolved or dispersed in a vehicle. The CETP immunogen comprises an immunogenic polypeptide having a CETP amino acid residue sequence that is covalently bonded to an exogenous antigenic polypeptide carrier. That carrier is selected from the group consisting of hepatitis B core protein (HBcAg), tetanus toxoid, tuberculin purified protein derivative (PPD), diphteria toxoid and branched oligolysine; and

(b) maintaining the immunized mammal for a time period sufficient for the immunogenic polypeptide to induce the production of antibodies that bind to CETP and lessen the transfer of cholesteryl esters from HDL. In one embodiment, the immunogenic polypeptide is an intact CETP molecule such as recombinant human or rabbit CETP. In another embodiment, the immunogenic polypeptide is a portion of a CETP molecule that is covalently bonded to an exogenous antigenic carrier.

HBcAg is particularly preferred as an exogenous antigenic carrier, and is more preferred when utilized as a fusion protein with the immunogenic polypeptide having an amino acid residue sequence of the carboxy-terminal 30 residues of CETP. That more preferred fusion protein constitutes a polypeptide having the amino acid residue sequence of the hepatitis B core antigen from which about 3 to about 53 amino acid

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residues have been deleted and replaced by the immunogenic polypeptide that more preferably still has a length about equal to the number of amino acid residues deleted from HBcAg. The resulting fusion protein is most preferably present in the inoculum as particles having the size of HBcAg particles (about 27 nm).

The present invention has several benefits and advantages. One salient benefit is that a contemplated process can be utilized to lessen the CE transfer from HDL to LDL or VLDL, thereby increasing the concentration of anti-atherogenic HDL cholesterol.

An advantage of the invention is that a contemplated process can have an effect that lasts for months as compared to the short-term effects of the small molecule drugs non available.

Another benefit of a contemplated process is that it utilizes the host mammal's own (autogeneic) immunological system to provide a desired result, thereby obviating problems associated with repeated administration of xenogeneic antibodies that themselves become immunogenic in the host mammal.

Another advantage of some contemplated processes is that their use of well known and accepted exogenous antigenic carriers such as HBcAg, tetanus toxoid, tuberculin PPD and diphtheria toxoid can boost the host mammal's immunity to those pathogens.

Still further benefits and advantages of the present invention will become apparent to a skilled worker from the disclosure that follows.

#### <u>Definitions</u>

The term "recombinant" is used to denote a version of a molecule made by a process by which a gene

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is cloned and expressed using recombinant DNA technology and genetic engineering in a bacterial, viral or mammalian host cells to produce an expressed protein in a recombinant form.

The term "polypeptide" is used herein to denote a sequence of about 10 to about 500 peptide-bonded amino acid residues. A whole protein as well as a portion of a protein having the stated minimal length are polypeptides.

The term "whole length CETP" is used to denote the full length CETP molecule (for example 476 amino acid residues long for human CETP or 496 residues long for rabbit CETP) as available in nature or produced as a recombinant protein.

The term "CETP immunogen" is used to denote molecule that is used to induce the production of antibodies that immunoreact with (bind to) CETP.

The terms "immunogenic polypeptide having a CETP amino acid residue sequence" or "immunogenic polypeptide" are used to denote the anti-CETP antibody-inducing portion of a "CETP immunogen"; i.e., that portion of a CETP immunogen to which induced antibodies bind.

The term "fusion protein" is used to denote the expression product of two or more different genes in which the amino acid residue sequences of both genes are expressed peptide-bonded together as a single molecule. It is noted that a fusion protein need not have the full length amino acid residue sequence of any protein, but rather usually contains two or more truncated sequences. The term is therefore somewhat of a misnomer, but is nonetheless well known and used as defined here by those skilled in the art.

The terms "exogenous antigenic carrier" or "carrier" is used herein to denote a molecule foreign to

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the immunized mammal that provides a signal to antibodyproducing B cells. Such carriers and their functions are well known in the art. Such a carrier can be a polypeptide having a sequence of as few as about 10 amino acid residues to the length of an intact protein, as well as being a synthetic polymer or oligomer.

The term "inoculum" in its various grammatical forms is used herein to describe a composition containing an amount of CETP immunogen (e.g., polypeptide conjugate, CETP protein or recombinant protein) sufficient for a described purpose that is dissolved or dispersed in an aqueous, physiologically tolerable diluent.

The term "expression" is used to mean the combination of intracellular processes, including transcription and translation undergone by a structural gene to produce a polypeptide.

The terms "operatively linked" or "operably inserted" are used to mean that two or more DNA sequences are covalently bonded together in correct reading frame.

The term "promoter" is used to mean a recognition site on a DNA sequence or group of DNA sequences that provide an expression control element for a gene and to which RNA polymerase specifically binds and initiates RNA synthesis (transcription) of that gene.

The term "recombinant DNA molecule" is used to mean a hybrid DNA sequence comprising at least two nucleotide sequences not normally found together in nature.

The term "structural gene" is used to mean a DNA sequence that is expressed as a polypeptide; i.e., an amino acid residue sequence.

The term "vector" is used to mean DNA molecule capable of replication in a cell and/or to which another DNA segment can be operatively linked so as to bring about replication of the attached segment. A plasmid is an exemplary vector.

The term "expression vector" is used to mean a DNA sequence that forms control elements that regulate expression of structural genes when operatively linked to those genes within a vector.

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## Detailed Description of the Invention

The present invention relates to a process for increasing the ratio of HDL cholesterol to LDL cholesterol in the blood of a treated mammal that has CETP in its blood, and that in humans leads to an amelioration of dyslipoproteinemias characterized by low HDL/LDL cholesterol ratios. That desired raising of the HDL/LDL cholesterol ratio is accomplished immunologically by antibodies induced in the blood of the treated mammal that recognize circulating CETP. Also contemplated in this invention are an immunogen utilized in the process, an inoculum that utilizes the immunogen and an isolated and purified DNA segment that encodes a contemplated immunogen.

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## I. The Process

A contemplated process is referred to herein as utilizing "autogeneic" antibodies to denote that the useful antibodies are those induced in the host mammal itself. This autogeneic immunological process is therefore to be distinguished from a xenogeneic process in which antibodies from an animal of one species are administered to an animal of another species as where the mouse anti-CETP TP2 or 1C4 monoclonal antibodies have been administered to hamsters or rabbits. A

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contemplated autogeneic immunological process is also to be distinguished from an allogeneic immunological process such as a passive immunization in which antibodies from one animal are administered to another animal of the same species as where humans receive gamma globulin injections from other humans.

A contemplated process is thus closely analogous to an autoimmune process in which a mammal's own immune system attacks an endogenous or self protein. CETP is an endogenous protein in rabbits, hamsters and primates that are among the mammalian hosts contemplated here. However, inasmuch as the cause of most if not all autoimmune responses is presently unknown and the desired immune response contemplated here is purposefully induced, it is believed appropriate to use a different name for the result obtained here.

Thus, one aspect of the present invention contemplates a process for lessening the transfer of cholesteryl esters from HDL particles and increasing the concentration of HDL cholesterol in the blood of a mammal whose blood contains cholesterol ester transfer protein (CETP). That process comprises the steps of:

(a) immunizing that mammal (the host) with an inoculum that contains a CETP immunogen dissolved or dispersed in a vehicle. The CETP immunogen is an immunogenic polypeptide having a CETP amino acid residue sequence. The immunized mammal is (b) maintained for a time period sufficient for the immunogenic polypeptide to induce the production of antibodies that bind to CETP and lessen the transfer of cholesteryl esters (CE) from HDL.

#### A. The CETP Immunogen

The immunogenic polypeptide having a CETP amino acid residue sequence of the CETP immunogen can be a whole CETP molecule such as the human (476 residues)

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or rabbit (496 residues) proteins whose amino acid residue sequences are provided as SEQ ID NOs:28 and 26, respectively, and whose DNA sequences are provided in SEQ ID NOs:1 and 27, respectively. The cDNA and deduced amino acid residue sequence for cynomolgus monkey CETP have also been reported by Pape et al., Atherosclerosis and Thrombosis, 11:1759-1771 (1991), and that polypeptide of SEQ ID NO:30 or a portion thereof as described below, can also be utilized herein, as can the cDNA of that monkey shown in SEQ ID NO:31 or a portion thereof.

Where the whole CETP molecule is used alone as the immunogenic polypeptide of the CETP immunogen, it is preferred to use a recombinant protein as compared to using protein recovered from an animal. It is also preferred to use a protein from an animal species other than that of the immunized mammal; i.e., the CETP used is preferably xenogeneic. An example of the use of a recombinant CETP protein from one animal in an immunized host mammal of another species is illustrated hereinafter by the use of recombinant human CETP in rabbits.

In an alternative procedure, a CETP protein is reacted with a plurality of diazotized sulfanilic acid molecules to form a modified CETP protein that itself serves as the CETP immunogen as is disclosed in U.S. Patent No. 4,767,842 for the human luteinizing hormone (HLH), whose disclosures are incorporated herein by reference. When this type of modification is utilized, the CETP protein used is preferably from the same species (allogeneic) as the immunized mammal.

When an immunogenic polypeptide is other than an intact CETP molecule, it is preferred to use a polypeptide having a length of about 10 to about 30 amino acid residues, and more preferably, a length of

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about 20 to 30 residues. In this instance, the immunogenic polypeptide is covalently bonded to an exogenous antigenic carrier to form the CETP immunogen. Several means are known in the art for covalently bonding polypeptides together, and several such means are discussed hereinafter. It is preferred that the covalent bond used to link the exogenous antigenic carrier and immunogenic polypeptide be a peptide bond. Several methods for forming peptide bonds are also well known in the art, but the preferred method of forming that bond is by expression of a fusion protein.

Exogenous antigenic carrier polypeptide molecules are also well known in the art, as are the amino acid residue and nucleotide sequences of those molecules. Exemplary polypeptide carriers include but are not limited to tetanus toxoid, tuberculin purified protein derivative (PPD), diphtheria toxoid, thyroglobulin and the hepatitis B core protein (HBcAq).

Thus, the cDNA encoding an exogenous antigenic carrier and that encoding an immunogenic CETP polypeptide can be operatively linked to form a single isolated and purified DNA molecule that encodes both the carrier and immunogenic polypeptide. That DNA molecule can then be operatively linked in an appropriate expression vector that expresses those two polypeptides as a single fusion protein whose two polypeptide portions are covalently bonded by a peptide bond. Preferably, the carrier is expressed at the aminoterminus of the fusion protein, although a carrier can also be expressed at the carboxy-fusion terminus of the immunogenic polypeptide. Exemplary proteins and procedures for their synthesis are discussed hereinafter.

Preferably, where the whole CETP molecule is used as the immunogenic polypeptide, the carrier

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polypeptide has an amino acid residue sequence that is less than that of a whole protein. That length is preferably about 15 to about 70 amino acid residues.

The hepatitis B nucleocapsid or core protein antigen also referred to as HBcAg is a particularly preferred exogenous antigenic carrier, as will be discussed in greater detail hereinafter. The HBcAg molecule will often be used herein illustratively as a carrier.

U.S. Patent No. 4,818,527, whose disclosures are incorporated by reference, teaches that the region extending from about position 70 through about position 140 from the amino-terminus of HBcAg, whose complete amino acid and cDNA sequences are shown as SEQ ID NOs:38 and 39, respectively, is particularly useful as a T cell independent stimulant as are sequences of about 15 to about 25 residues from that region. The amino acid residue sequences of four of those shorter polypeptides are provided as SEQ ID NOs:40, 41, 42 and 43. sequences that encode each of those four polypeptides can be readily obtained from SEQ ID NO:39, and the 3' end of such a cDNA can be operatively linked to the 5' end of cDNA that encodes an immunogenic polypeptide, or vice versa, for expression as a fusion protein CETP immunogen.

Thus, in one embodiment, a preferred CETP immunogen is a fusion protein whose amino-terminal portion is a polypeptide having a length of about 15 to about 70 amino acid residues and having the sequence of HBcAg from about position 70 to about position 140 from the HBcAg amino-terminus. The carboxy-terminal portion of that fusion protein has the amino acid residue sequence of a CETP molecule, and the two portions are covalently bonded by a peptide bond. In this

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embodiment, the CETP molecule can be from the same species as the immunized mammal.

In another preferred embodiment, the CETP immunogen is comprised of an exogenous antigenic carrier to which one or more immunogenic polypeptides having a length of about 10 to about 30 amino acid residues such as those of SEQ ID NOs:2-7 or 50 having a sequence of rabbit CETP, the similar polypeptides of SEQ ID NOs:8-13 or 29 having a sequence of human CETP or the similar polypeptides of SEQ ID NOs:32-37 having a sequence of monkey CETP is covalently bonded. Here, the carrier is preferably an intact protein such as a before-noted tetanus toxoid, tuberculin PPD, diphtheria toxoid, thyroglobulin or HBcAg molecule or a synthetic carrier such as the branched oligolysine described in Tam et al., Proc. Natl. Acad. Sci., USA, 86:9084-9088 (1989) or the similarly prepared branched oligolysine that is also linked to resin particles as described in Butz et al., Pep Res. 7(1):20-23.

Methods for covalent bonding of an immunogenic polypeptide are extremely varied and are well known by workers skilled in the immunological arts. For example, following U.S. Patent No. 4,818,527, whose disclosures are incorporated hereinby reference, m-maleimidobenzoyl-N-hydoxysuccinimide ester (ICN Biochemicals, Inc.) or succinimidyl 4-(N-maleimidomethyl)cyclohexane-1carboxylate (SMCC, Pierce) is reacted with HBcAg to form an activated carrier. That activated carrier is then reacted with a polypeptide of SEQ ID NOs: 2-7, 8-13, 29, 32-37 or 50 to which an additional amino- or carboxyterminal cysteine residue has been added to form a covalently bonded CETP immunogen as a conjugate. Alternatively, the amino group of an immunogenic polypeptide can be first reacted with N-succinimidyl 3-(2-pyridylthio)propionate (SPDP, Pharmacia), and that

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thiol-containing polypeptide can be reacted with the activated carrier after reduction. Of course, the sulfur-containing moiety and double bond-containing Michael acceptor can be reversed. These reactions are described in the supplier's literature, and also in Kitagawa et al., J. Biochem., 79:233 (1976) and in P.J. Lachmann et al., in 1986 Synthetic Peptides As Antigens, Wiley, Chichester, (Ciba Foundation Symposium 119) pages 25-40.

Previously discussed U.S. Patent No. 4,767,842 also teaches several modes of covalent attachment between a carrier and polypeptide that are useful here. In one method, tolylene diisocyanate is reacted with the carrier in a dioxane-buffer solvent at zero degrees C to form an activated carrier. An immunogenic polypeptide such as those of SEQ ID NOs:2-7, 8-13, 29, 32-37 or 50 is thereafter admixed and reacted with the activated carrier to form the CETP immunogen as a covalently bonded conjugate.

An exemplary antigenic carrier protein is the purified protein derivative (PPD) of tuberculin. Exemplary use of this carrier is discussed in P.J. Lachmann et al., in 1986 Synthetic Peptides As Antigens, Wiley, Chichester (Ciba Foundation Symposium 119) pages 25-40. Briefly, PPD is prepared from culture supernatants of Mycobacterium tuberculosis by ultrafiltration, heating to 100°C and precipitation with trichloroacetic acid, and is available from commercial sources. This carrier is particularly useful for immunizing mammalian host animals that have been primed with Bacillus Calmatle-Guerin (BCG), as are humans who have been immunized against the tubercle bacillus.

In an exemplary coupling, PPD is thiolated using SPDP as described by the reagent's manufacturer. This technique can provide up to about five thiol-groups

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per PPD molecule. An immunogenic polypeptide such as those of SEQ ID NOs:2-7, 8-13, 29, 32-37 or 50 is coupled via its amino-terminal amine to SMCC, and after reduction of the thiolated PPD, the thiolated PPD and SMCC-reacted peptide are reacted as described by the reagent manufacturers to form a CETP immunogen as a covalently bonded conjugate.

An immunogenic polypeptide having a length of about 10 to about 30 amino acid residues, when desired as a free molecule, is usually most easily made by solid phase synthesis techniques, as are well known. Several such techniques are noted or cited in U.S. Patent No. 5,582,997, whose disclosures are incorporated herein by reference.

Where a longer immunogenic polypeptide is desired, or where the immunogenic polypeptide is a portion of a CETP immunogen that is a fusion protein, it is preferred to utilize recombinant DNA synthetic techniques. DNA sequences for the CETP molecule or a desired portion thereof can be obtained as described by M.E. Pape et al., Arteriosclerosis and Thrombosis, 11:1759-1771 (1991); N.W. Jeong et al., Mol. Cells, 4(4):529-533 (1994); and D.T. Connolly et al., Biochem. J., 320:39-47 (1996). Oligonucleotides can also be prepared using standard synthetic technology where shorter DNA sequences are desired. Those oligonucleotides can also be linked enzymatically, as with T4 DNA ligase, to form longer molecules.

DNA sequences for exogenous antigenic carrier molecules have also been reported as have methods for expressing those molecules. For example, a DNA sequence that encodes the preferred HBcAg exogenous antigenic carrier is disclosed in U.S. Patent No. 4,710,463, whose disclosures are incorporated herein by reference, and E. coli-containing plasmids whose DNA encode hepatitis B

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virus proteins were deposited in the Culture Collection of the National Collection of Industrial Bacteria, Aberdeen Scotland as pBR322-HBV G-L. In addition, DNA encoding HBcAg is disclosed in U.S. Patent No. 4,942,125 as present in vectors deposited at the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, MD 20852-1776 as ATCC No. 39629, No. 39631 and No. 40102.

The use of HBcAg as an exogenous antigenic carrier in a fusion protein is illustrated in Moriarty et al., Vaccines 90, Brown et al. eds., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 225-229 (1990). The authors there reported operatively linking the 3' end of DNA encoding a 17-mer amino acid residue sequence of the HIV gag protein to the 5' end of DNA encoding HBcAg, and reported that appropriately transfected E. coli expressed a fusion protein having the HIV gag sequence peptide-bonded to the aminoterminus of HBcAg. That expressed fusion protein was present in particulate form and was shown to be an excellent immunogen in mice.

Schödel et al., Vaccines 90, Brown et al. eds., Cold Spring Harbor Laboratory Press, 193-198 Cold Spring Harbor, N.Y. (1990) reported the preparation and successful use of a fusion protein immunogen that contained a polypeptide immunogen having an amino acid residue sequence of hepatitis B Pre-S2 (residues 133-140) that was expressed peptide-bonded to the carboxy-terminus of HBcAg so that the 3' end of the exogenous carrier (HBcAg) DNA was linked to the 5' end of the DNA that encoded the Pre-S2 polypeptide immunogen. That expressed fusion protein immunogen was also obtained in particulate form.

Similar techniques can be utilized here using a DNA molecule of SEQ ID NOs:14-19, 20-25 or a

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corresponding DNA sequence of SEQ ID NO:31 that encodes a CETP immunogenic polypeptide in place of the DNAs used by the Moriarty et al. or the Schödel et al. groups.

In addition, using similar techniques and others well known to workers of ordinary skill in the recombinant DNA art, a fusion protein can be prepared having an HBcAg amino acid residue sequence such as one of those of SEQ ID NOs:40-43 peptide-bonded to the amino-terminus of an intact CETP molecule.

A particularly preferred CETP immunogen is a fusion protein comprised of an immunogenic polypeptide having a length of 10 to about 30 amino acid residues that is peptide bonded to both an amino-terminal flanking amino acid residue sequence and a carboxy-terminal flanking sequence, and is sometimes referred to hereinafter HBcAg/CETP/HBcAg. Those flanking sequences are preferably portions from the amino-terminal and carboxy-terminal regions of the HBcAg molecule, as was discussed previously. Thus, in this fusion protein, the exogenous antigenic carrier molecule is peptide-bonded to both the amino-terminus and carboxy-terminus of the immunogenic polypeptide.

A preferred polypeptide immunogen has an amino acid residue sequence of SEQ ID NOs:2-7, 8-13, 29, 32-37 or 50. Most preferably, the polypeptide immunogen has an amino acid residue sequence that is bound by (immunoreacts with) the monoclonal antibodies designated TP1, TP2 and TP3 reported by B. Hessler et al., J. Biol. Chem., 263(11):5020-5023 (1988), or that denominated 1C4 by J. Gaynor et al., Atherosclerosis, 110(1):101-109 (1994). Monoclonal antibody TP2 binds to an epitope located between about positions 465 and 475 of human CETP. Tall, J. Lipid Res., 34:1255-1274 (1993), and the citations therein.

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A particularly preferred polypeptide immunogen has an amino acid residue sequence that includes positions 465 through 475 of human CETP or an analogous position of CETP from another source, and is exemplified by the polypeptides of SEQ ID NOs:4, 10 and 34, as well as SEQ ID NO:29, of which the polypeptides of SEQ ID NO:10 NOs:10 and 29 are most preferred, with SEQ ID NO:10 being encoded by the DNA of SEQ ID NO:22.

Protein molecules have not only a linear amino acid residue or primary sequence, but also can possess a secondary sequence in which the polypeptide back bone is coiled in an  $\alpha$ -helix or folded into a  $\beta$ -sheet, as well as a tertiary sequence in which sequentially distant portions of the molecule are folded to be adjacent to each other. Many linear antigenic/immunogenic polypeptide sequences have been reported in the literature, and such sequences can be readily mimicked by polypeptides having a length of 10 to about 30 amino acid residues. Such relatively short polypeptides typically do not mimic a secondary structure such as an  $\alpha$ -helix in aqueous media.

The region of CETP that immunoreacts with monoclonal antibody TP2 is predicted to have an amphipathic helical secondary structure, with the hydrophilic surface bound by the antibody. See Wang et al., J. Biol. Chem., 267(25):17487-17490 (1992) and A.R. Tall, J. Lipid Res. <u>34</u>:1255-1274 (1993). A contemplated CETP immunogen fusion protein having an immunogenic polypeptide flanked at its amino- and carboxy-termini by peptide-bonded regions of HBcAg; i.e., HBcAg/CETP/HBcAg, is more constrained in its molecular motions than is an immunogenic polypeptide that is bonded at only one terminus. As a consequence, by flanking a beforementioned particularly preferred immunogenic polypeptide with regions of HBcAg to form a HBcAg/CETP/HBcAg fusion

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protein, it is believed that the immunogenic polypeptide becomes constrained to have a helical structure much like that present in the native CETP molecule and thereby induce autogeneic antibodies having an antigenic specificity similar to those exhibited by mouse monoclonal antibodies TP1, TP2, TP3 and 1C4 discussed previously.

It is further believed that formation of HBcAg-like particles of a contemplated fusion protein HBcAg/CETP/HBcAg immunogen places further conformational constraints upon the immunogenic polypeptide by which the immunogenic polypeptide becomes the primary immunogen with loss of much of the HBcAg immunogenicity, while the T cell-independent antigenic carrier function of HBcAg is retained. See Schödel et al., J. Virol., 66(1):106-114 (1992) for a similar result using a different immunogen.

Although use of the full length HBcAg exogenous antigenic carrier molecule or substantially full length molecule has thus far been discussed, it is noted that about 10 amino-terminal amino acid residues or about 40 carboxy-terminal amino acid residues can be deleted from the expressed HBcAg/CETP/HBcAg sequence without abrogating function as an exogenous antigenic carrier or assembly into particles. See, for example, Birnbaum et al., J. Virol., 64(7):3319-3330 (1990).

Exemplary preparations of immunogenic fusion proteins having HBcAg as a carrier with various heterologous polypeptide insertions from pathogens as immunogen, and also usage of full length and carboxyterminal deletions in the HBcAg amino acid residue sequence can be found in the following publications. Schödel et al., J. Exp. Med., 180:1037-1046 (1994); Schödel et al., J. Virol., 66(1):106-114 (1992); Schödel et al., Vaccines 91, Brown et al. eds., Cold Spring

Harbor Laboratory Press, Cold Spring Harbor, N.Y., 319-325 (1991); Clarke et al., Vaccines 91, Brown et al. eds, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 313-318 (1991); and Schödel et al., Vaccines 90, Brown et al. eds., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 193-198 (1990).

It is also noted that the human hepatitis virus (HBV), whose core antigen is discussed herein, has two subtypes that are denominated adw and ayw. The core antigens of those two viral subtypes have slightly different DNA and amino acid residue sequences. Although subtype specificity has been noted as to the immunogenicity of the S and PreS regions of HBV, [see, for example, Milich et al. Vaccines 86, Brown et al. eds., Cold Spring Harbor Press, Cold Spring Harbor, N.Y., 377-382 (1986)] either subtype can be used as an exogenous antigenic carrier herein, with subtype ayw being used illustratively herein.

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### B. <u>Inocula</u>

A CETP immunogen is dissolved or dispersed in a pharmaceutically acceptable vehicle composition that is preferably aqueous to form an inoculum that, when administered to a mammal whose blood contains CETP in an effective amount, induces the production of antibodies that immunoreact with (bind to) CETP and lessen the transfer of cholesteryl esters from HDL particles.

Inocula typically contain CETP immunogen concentrations of about 10 micrograms to about 500 milligrams per inoculation (unit dose), and preferably about 50 micrograms to about 50 milligrams per unit dose. The term "unit dose" as it pertains to an inoculum of the present invention refers to physically discrete units suitable as unitary dosages for animals,

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each unit containing a predetermined quantity of active material calculated to individually or collectively produce the desired immunogenic effect in association with the required diluent; i.e., carrier, or vehicle.

Inocula are typically prepared from a dried solid CETP immunogen by dispersing the immunogen in a physiologically tolerable (acceptable) diluent vehicle such as water, saline phosphate-buffered saline (PBS), Ringer's solution or the like to form an aqueous composition. The diluent vehicle can also include oleaginous materials such as peanut oil, squalane or squalene as is discussed hereinafter. The amount of CETP immunogen utilized in each immunization can vary widely, and is referred to as an effective amount. an effective amount is sufficient to induce antibodies to CETP that bind to CETP and lessen the transfer of cholesteryl esters from HDL particles. Exemplary effective amounts of CETP immunogen are about 500  $\mu$ q to about 500 mg, depending inter alia, upon the CETP immunogen, mammal immunized, and the presence of an adjuvant in the inoculum, as discussed below. single unit dose or a plurality of unit doses can be used to provide an effective amount of CETP immunogen.

Inocula can also include an adjuvant as part of the diluent. Adjuvants such as complete Freund's adjuvant (CFA) that is not used in humans, incomplete Freund's adjuvant (IFA) and alum are materials well known in the art, and are available commercially from several sources. The use of small molecule adjuvants is also contemplated herein.

Exemplary of one group of small molecule adjuvants are the so-called muramyl dipeptide analogues described in U.S. Patent No. 4,767,842. Another type of small molecule adjuvant described in U.S. Patent No. 4,787,482 that is also useful herein is a 4:1 by volume

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mixture of squalene or squalane and  $Arlacel^{M}$  A (mannide monooleate).

Yet another type of small molecule adjuvant useful herein is a 7-substituted-8-oxo or sulfo-guanosine derivative described in U.S. Patents No. 4,539,205, No. 4,643,992, No. 5,011,828 and No. 5,093,318, whose disclosures are incorporated by reference. Of these materials, 7-allyl-8-oxoguanosine (loxoribine) is particularly preferred. That molecule has been shown to be particularly effective in inducing an antigen-(immunogen-)specific response.

Adjuvants are utilized in an adjuvant amount, which can vary with the adjuvant, mammal and CETP immunogen. Typical amounts can vary from about 100  $\mu g$  to about 200 mg per immunization. Those skilled in the art know that appropriate concentrations or amounts can be readily determined.

An inoculum is typically formulated for parenteral administration. Exemplary immunizations are carried out sub-cutaneously (s.c.) intra-muscularly (i.m.) or intra-dermally (i.d.).

Once immunized, the mammal is maintained for a period of time sufficient for the CETP immunogen to induce the production of antibodies that bind to CETP and lessen the transfer of cholesteryl esters from HDL particles. This maintenance time typically lasts for a period of about three to about eight weeks, and can include a booster, second immunizing administration of the inoculum.

The production of antibodies that bind to CETP is readily ascertained by obtaining a plasma or serum sample from the immunized mammal and assaying the antibodies therein for their ability to bind to CETP as an antigen in an ELISA assay as described hereinafter,

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or by another immunoassay such as a Western blot as is well known in the art.

The lessening of transfer of cholesteryl esters from HDL can be assayed by one or more of several In one assay, the rate of transfer is techniques. measured by use of a  $[^{3}H]$ -cholesteryl ester ( $[^{3}H]$ CE) from HDL to LDL following the differential precipitation assay reported by Glenn et al., Methods in Enzymology, 263:339-350 (1996). Briefly, in a volume of 200  $\mu$ l, CETP, [3H]CE-labeled HDL, LDL, and TES assay buffer (50 mM Tris, pH 7.4; 150 mM NaCl; 2 mM EDTA; 1% bovine serum albumin) are incubated for 2 hours at 37°C in 96-well filter plates. LDL is then differentially precipitated by the addition of 50  $\mu$ l of 1% (w/v) dextran sulfate/0.5  $M MgCl_2$ . After filtration, the radioactivity present in the precipitated LDL is measured by liquid scintillation counting. Correction for non-specific transfer or precipitation is made by including samples that did not contain CETP. The rate of [3H]CE transfer using this assay is linear with respect to time and CETP concentration. For studies in which antibodies are included in the assay, the order of addition into sample wells is: buffer, [3H]CE-labeled HDL, LDL, antibodies, CETP.

methods that do not involve differential precipitation. In the first assay, the incubation conditions are identical to those described above, but separation of LDL acceptor particles from [³H]CE-labeled HDL donor particles is accomplished by size exclusion chromatography on tandem columns of Superose™ 6 (Sigma Chemical Co.), followed by liquid scintillation counting of fractions to determine the amount of [³H]CE associated with LDL and HDL. The amount of transfer

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measured by this method is typically in excellent agreement with the precipitation assay.

The third assay for CETP activity measures the rate of CETP-mediated transfer of the fluorescent analog NBD-cholesteryl linoleate (NBD-CE) from an egg phosphatidyl choline emulsion to VLDL. This assay takes advantage of the fact that NBD-CE is self-quenched when in the emulsion, and becomes fluorescent when transferred to VLDL. The assay is carried out according to the manufacturer's instructions (Diagnescent Technologies Inc., Yonkers, New York). Fluorescence measurements can be taken using a standard machine such as an SLM 8000C spectrophotofluorometer (Milton Roy Co., Rochester, New York) using 465 nm and 535 nm for excitation and emission wavelengths, respectively.

It is particularly contemplated once the desired antibodies are induced in the mammal that the immunization step be repeated at intervals of about 3 to about 6 months until the HDL cholesterol value in the blood of the mammal is increased by about 10 percent or more relative to the HDL cholesterol value for the mammal prior to the first immunization step. Preferably, the HDL cholesterol value is increased by about 25 percent. The mammal is thereafter preferably maintained at that increased HDL cholesterol level by periodic booster immunizations administered at intervals The increase in HDL of about 9 to about 18 months. cholesterol can be measured by any reliable assay, many of which are well known in the art, and one of which is described hereinafter.

It is noted that the before-described anti-CETP antibodies so induced can be isolated from the blood of the host mammal using well known techniques, and then reconstituted into a second inoculum for passive immunization as is also well known. Similar

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techniques are used for gamma-globulin immunizations of humans. For example, antiserum from one or a number of immunized hosts can be precipitated in aqueous ammonium sulfate (typically at 40-50 percent of saturation), and the precipitated antibodies purified chromatographically as by use of affinity chromatography in which CETP or an immunogenic polypeptide portion thereof is utilized as the antigen immobilized on the chromatographic column.

## C. DNA Molecules and Expression Systems

A contemplated DNA molecule (isolated purified DNA segment) that encodes a CETP immunogen can be referred to as a number of base pairs at a particular location in a plasmid, as a restriction fragment bounded by two restriction endonuclease sites, and as a restriction fragment bounded by two restriction endonuclease sites and containing a number of base pairs. A contemplated DNA can also be defined to have a sequence of a denominated SEQ ID NO, as well as alleles or variants of such genes (described hereinafter) that encode a recited amino acid residue sequence.

A contemplated isolated and purified DNA segment is linear, and as such has a 5' end and a 3' end. A contemplated DNA segment can comprise two or more individual DNA segments whose 3' ends are operatively linked to the 5' end of another DNA segment where two segments are joined, or whose 3' end is operatively linked to the 5' end of another DNA segment whose own 3' end is operatively linked to the 5' end of yet another DNA segment, where three individual segments are joined to form a single isolated and purified DNA segment.

In living organisms, the amino acid residue sequence of a protein or polypeptide is directly related via the genetic code to the deoxyribonucleic acid (DNA)

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sequence of the structural gene that codes for the protein. A structural gene can be defined in terms of the amino acid residue sequence; i.e., protein or polypeptide, for which it codes.

In addition, through the well-known redundancy of the genetic code, additional DNA sequences can be prepared that encode the same amino acid residue sequences, but are different from a recited gene sequence having a particular SEQ ID NO. For example, in vitro mutagenesis as is illustrated hereinafter can be used to change a DNA sequence so that the same residue of an expressed polypeptide is expressed using one or more different codons. In addition, that same technique can be used to change one amino acid residue to another where it is desired to insert or delete specific restriction endonuclease sites. This technique is also illustrated hereinafter.

A DNA sequence that encodes a CETP immunogen of a recited SEQ ID NO but has a DNA sequence different from that of a recited SEQ ID NO is referred to herein as a variant DNA sequence. Such a variant DNA molecule can be readily prepared by in vitro mutagenesis, as is well known.

A DNA segment that encodes a described CETP immunogen can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci et al., J. Am. Chem. Soc., 103:3185 (1981). Of course, by chemically synthesizing the coding sequence, any desired modifications can be made simply by substituting the appropriate bases for those encoding the native amino acid residue sequence.

However, DNA segments including the specific sequences discussed previously are preferred. Furthermore, a DNA segment that encodes a polypeptide

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can be obtained from a recombinant DNA molecule (plasmid or other vectors) containing that segment.

A DNA segment that includes a DNA sequence encoding a CETP immunogen can be prepared by excising and operatively linking appropriate restriction fragments from appropriate plasmids or other DNA using well known methods. The DNA molecules useful here that are produced in this manner typically have cohesive termini; i.e., "overhanging" single-stranded portions that extend beyond the double-stranded portion of the molecule. The presence of cohesive termini on the DNA molecules of the present invention is preferred, although molecules having blunt termini are also contemplated.

A recombinant DNA molecule useful herein can be produced by operatively linking a vector to an isolated DNA segment that encodes a CETP immunogen to form a plasmid such as those discussed herein. Particularly preferred recombinant DNA molecules are discussed in detail in the examples, hereafter. Vectors capable of directing the expression of the gene are referred to herein as "expression vectors".

The expression vectors described above contain expression control elements including a promoter. The genes that encode an immunogenic polypeptide or other useful sequence are operatively linked to the expression vector to permit the promoter sequence to direct RNA polymerase binding and expression of the desired polypeptide coding gene. Useful promoters for expressing the polypeptide coding gene are inducible.

The choice of which expression vector to which a polypeptide-coding gene is operatively linked depends directly on the functional properties desired, e.g. the location and timing of protein expression, and the host cell to be transformed. These are well known

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limitations inherent in the art of constructing recombinant DNA molecules. However, a vector useful in practicing the present invention is capable of directing the replication and also the expression of the immunogenic polypeptide-coding gene included in the DNA segment to which it is operatively linked.

In one preferred embodiment, a vector includes a prokaryotic replicon; i.e., a DNA sequence having the ability to direct autonomous replication and maintenance of the recombinant DNA molecule extrachromosomally in a prokaryotic host cell transformed therewith. Such replicons are well known in the art.

Those vectors that include a prokaryotic replicon can also include a prokaryotic promoter region capable of directing the expression of the CETP immunogen gene in a host cell, such as *E. coli*, transformed therewith. Promoter sequences compatible with bacterial hosts are typically provided in plasmid vectors containing one or more convenient restriction sites for insertion of a DNA segment of the present invention. Typical of such vector plasmids are pUC18, pUC19, and pBR322 available from Gibco BRL, Gaithersburg, MD, and pPL and pKK223-3 available from Pharmacia, Piscataway, N.J. These vectors are utilized in the synthesis of the DNA segments useful herein.

In preferred embodiments, the vector used to express an immunogenic polypeptide-coding gene includes a selection marker that is effective in a host cell, preferably a drug resistance selection marker. One preferred drug resistance marker is the gene whose expression results in kanamycin resistance, whereas ampicillin resistance is another such marker. Again, such selective markers are well known.

A variety of methods has been developed to operatively link DNA to vectors via complementary

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cohesive termini or blunt ends. For instance, complementary homopolymer tracts can be added to the DNA segment to be inserted and to the vector DNA. The vector and DNA segment are then joined by hydrogen bonding between the complementary homopolymeric tails to form recombinant DNA molecules.

Alternatively, synthetic linkers or adapters containing one or more restriction endonuclease sites can be used to join the DNA segment to the integrating expression vector. The synthetic linkers or adapters are attached to blunt-ended DNA segments by incubating the blunt-ended DNA segments with a large excess of synthetic linker or adapter molecules in the presence of an enzyme that is able to catalyze the ligation of blunt-ended DNA molecules such as bacteriophage T4 DNA ligase.

Thus, the products of the reaction are DNA segments carrying synthetic linker sequences at their ends. These DNA segments are then cleaved with the appropriate restriction endonuclease and ligated into an expression vector that has been cleaved with an enzyme that produces termini compatible with those of the synthetic linker. Synthetic linkers containing a variety of restriction endonuclease sites are commercially available from a number of sources including New England BioLabs, Beverly, MA. A synthetic adapter molecule typically has sticky end and one blunt end and is not cleaved after ligation.

Although preferred, it is not always feasible to design a DNA molecule whose expressed polypeptide has the exact terminal residues of a polypeptide enumerated in a SEQ ID NO. This is because of the limitations inherent in the use of restriction enzymes, synthetic linkers and adapter molecules used for cutting and joining DNA segments.

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As a consequence, an expressed polypeptide can contain a few (e.g. one or two) more, less or different amino acid residues at one or both termini of an enumerated sequence. Such slight changes are well tolerated by a contemplated CETP immunogen, particularly when the substitution is conservative and residues such as Cys and Pro are avoided.

# Best Mode for Carrying Out The Invention

10 Example 1: Immunization Of Rabbits With Rabbit CETP-Peptides

There is a 88 percent homology between rabbit and human CETP at the amino acid residue level. Rabbits express high levels of CETP in their blood and were chosen as a model for illustrating production of autogeneic anti-CETP antibodies.

The six rabbit CETP polypeptides of SEQ ID NO:2-7 were selected for this study and were prepared by standard solid phase synthesis procedures discussed below. To enhance the anti-polypeptide-specific antibody responses, two separate immunization strategies were used with the above six rabbit CETP-polypeptides.

# A. <u>Immunization Strategy 1 (MAP conjugates)</u>

Rabbit polypeptides were synthesized as multiple antigenic peptide (MAP) constructs [D. N. Posnett et al., J. Biol Chem., 263:1719-1725 (1988)]. Those polypeptides were separately covalently bonded to "oligolysine core" molecules that were themselves covalently attached to resin particles [S. Butz et al., Pep. Res. 1:20-223 (1994)].

The substitution of the starting resin particles was 0.37  $\mu m$  sites/mg resin that provided approximately 500  $\mu g$  of immunogenic polypeptide per 1.1 mg resin. For the preparation of the CETP immunogen for immunization, 3.0 mg of dry resin were weighed out and hydrated in 1.3 ml sterile phosphate-buffered saline

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(PBS; pH 7.4) to which 1.3 ml Freund's complete adjuvant (CFA; Sigma Chemical Co., St. Louis, MO., F-5881) were added as adjuvant. The CETP immunogen and adjuvant were emulsified by a female-female luer lock syringe adapter connected to two 3 ml syringes. Each final emulsion was divided into 1.0 ml aliquots for injection (1 ml/rabbit), with one immunogen used per rabbit. Pre-immune rabbit serum was collected before immunization and stored at -70°C until immunoassay. On day 1, New Zealand white rabbits were separately immunized with respective immunogens by sub-cutaneous (s.c.) route on the back of the rabbit using 10 injection sites.

Three weeks later (on Day 22), the rabbits were boosted using similar procedures, but this time CETP immunogens were emulsified in Freund's incomplete adjuvant (IFA; Sigma). The resin-bonded CETP immunogen was weighed out as before and hydrated with sterile PBS the day before the booster immunization. The resulting CETP immunogen suspension was sonicated with a microtip at maximum setting for 5 minutes and left overnight (about 18 hours) at 4°C. Before mixing the hydrated CETP immunogen suspension with IFA, the suspension was warmed to room temperature just before the booster immunization, added to 1.5 ml IFA, and emulsified as described above to form an inoculum in which the CETP immunogen was dispersed. Rabbits were immunized each with 1 ml of emulsion in at least 10 injection sites s.c.

The first post-immune serum was collected 2 weeks after the second immunization from each animal. All the anti-sera samples were stored in -70°C until ELISA was done.

Using this MAP strategy, polypeptides of SEQ ID NOs:2 and 7 were moderately immunogenic in rabbits

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and resulted in maximum autogeneic antibody titers of 1:1000 and 1:300, respectively. The titers represent the dilution of the sera that gave a half maximal absorbance on ELISA plates coated with the respective polypeptides. Sera were pooled from two rabbits, and the above titers represent the mean value. Only antisera to SEQ ID NO:7 cross-reacted with recombinant human CETP. The reactivity of these anti-sera with rabbit CETP is under evaluation using various immunological assays. Anti-polypeptide-specific IgG has been purified from the post-immune sera and its inhibitory property on human recombinant CETP is being assayed.

# B. Immunization Strategy 2 (Purified Protein Derivative Conjugates)

Five of the above six rabbit CETP-polypeptide immunogens (SEQ ID NOs:2, 3, 4, 6 and 7) were coupled to tuberculin purified protein derivative (PPD) according to the teachings of P.J. Lachmann et al., in 1986 Synthetic Peptides As Antigens, (Ciba Foundation Symposium 119), 25-40 (1986) and P. Dawson et al., J. Bio. Chem., 264:16798-16803 (1989) to form a conjugate. The tuberculin PPD (Statens Serum Inst., Copenhagen, Denmark) was used as an exogenous antigenic carrier to enhance the immunogenicity of rabbit CETP-derived polypeptides. The polypeptide-PPD conjugate in PBS was emulsified with CFA as described for immunization strategy 1. One ml of 0.5 mg/ml polypeptide conjugated to PPD was emulsified with approximately 1 ml CFA. A second 1 ml PPD-conjugate was frozen for next booster immunization.

On Day 1, rabbits were immunized with 1 ml of final emulsion in at least 10 sites sub-contaneously on back of the rabbit. The polypeptide-PPD CETP polypeptide immunogen dose contained 0.25 mg of polypeptide per rabbit. Three weeks later (on Day 21), the rabbits were given the booster immunization dose

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3.0

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with the remaining 1 ml conjugate thawed and emulsified with IFA, as discussed before. Two weeks following the second immunization rabbits were bled to collect post-immune sera.

The PPD conjugation strategy resulted in antibodies to the immunogenic polypeptides of SEQ ID NOs:2 and 6, with antibody titers of 1:3200 and 1:400 respectively. The titers represent the dilution of the sera that gave a half maximal absorbance on peptide coated ELISA plates. Sera were pooled from two rabbits and represent the mean value. Only the antibodies to the immunogenic polypeptide of SEQ ID NO:2 cross-reacted with recombinant human CETP. These results were unexpectedly good inasmuch as P.J. Lachmann et al., supra, obtained substantially no anti-polypeptide antibodies in BCG-naive hosts as were these rabbits. Anti-PPD antibodies were detected in all groups of rabbits as expected.

Using ELISA, the anti-immunogenic polypeptide sera are being used to evaluate their immuno-reactivity with natural rabbit CETP. Because the polypeptides of SEQ ID NOs:2, 6 and 7 were immunogenic and the two anti-polypeptide antibodies against SEQ ID NOs:2 and 7 immunologically cross-reacted with recombinant human CETP, the respective rabbits were further boosted with a third immunization dose either with the MAP constructs or PPD constructs emulsified with IFA.

# Example 2: Immunization Of Outbred Rabbits With CETP-Based Antiqen

This study utilized 30 New Zealand white rabbits in three groups with 10 rabbits per group. Three immunogens were utilized in this study: (1) Recombinant human CETP, (2) the carboxy-terminal 26 amino acid residues of rabbit CETP (SEQ ID NO:50), and

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(3) a control immunogen whose amino acid residue sequence was unrelated to that of CETP.

Pre-immune sera were collected before immunization with the respective immunogens. The purpose of this study was to illustrate that the above CETP immunogens would induce anti-CETP-specific (autogeneic anti-CETP) antibodies in rabbits, and that the autogeneic antibodies generated against CETP bind to (immunoreact with) the endogenous rabbit CETP, and thus lessen the transfer of cholesteryl esters from HDL particles and raise the level of HDL in the hosts.

The above immunogens were emulsified in CFA. Each rabbit received 500  $\mu g$  of one of the immunogens emulsified in CFA immunized by sub-cutaneous route. Seven weeks later the first bleed post-immune sera were collected.

ELISA was employed to titrate the antibodies. ELISA plates were coated (40 ng/well) with the recombinant human CETP.

The rabbits immunized with recombinant human CETP exhibited a primary immune response against human CETP. All the ten rabbits responded well to the recombinant human CETP (rhCETP). The specific IgG antibody titer was >1:1000. However, the group of 10 rabbits immunized with the rabbit CETP carboxy-terminal polypeptide-thyroglobulin conjugate (CETP-TH) did not exhibit a primary antibody response. The control rabbit sera had no detectable levels of anti-CETP antibodies. The rabbits were boosted with each respective antigen to further study immunogenicity.

The results of this study on the elevation of HDL particle concentration in the blood (plasma) of the host mammals (mean  $\pm$ .S.D.) are shown in Table 1, below, for those first-immune sera.

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Table 1

HDL Levels In Immunized

Animals (mg/dl)

Immunogen	Avg.³ <u>HDL</u>	S.D.4	_ P <sup>5</sup> _
Control	23.89	3.92	<del></del>
$\mathtt{rhCETP}^\mathtt{1}$	26.59	4.41	0.17
CETP-TH2	26.14	6.93	0.38
	Control rhCETP <sup>1</sup>	Immunogen HDL  Control 23.89  rhCETP¹ 26.59	Immunogen         HDL         S.D. <sup>4</sup> Control         23.89         3.92           rhCETP <sup>1</sup> 26.59         4.41

- - <sup>2</sup> CETP-TH = C-terminal 26 rabbit CETP amino acid residues conjugated to thyroglobulin.
- <sup>3</sup> Avg. HDL = Average HDL concentration after immunization or mock immunization for the control.
  - <sup>4</sup> S.D. = Standard deviation.
- P = p value from a Student's T test analysis.

As can be seen from those results, an increase in HDL particle concentration was found after administration of each of the CETP immunogens. There was a relatively large scatter in the data.

Nevertheless, an approximately 10 percent increase in the HDL particle level was observed with each CETP immunogen as compared with the control, with the recombinant human CETP immunogen providing its increase at a confidence level of greater than 80 percent (p=0.17) using a Student's T test to analyze the results.

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Example 3: Construction Of E. coli Expression Vectors Encoding HBcAg/CETP/HBcAg
Chimeric Fusion Proteins

## A. PCR amplification of HBcAq

Plasmid pFS14, a derivative of expression vector pKK223 (Pharmacia), encodes HBcAg (subtype ayw) [Schödel et al., Infect. Immun. 57:1347 (1989)]. PCR primer A, below, is designed to amplify the 5' end of HBcAg and place an NcoI (C'CATG,G) site in the correct reading frame at the natural ATG start codon. In each of the sequences shown hereinafter, only the coding strand is shown, and bases removed after cleavage by restriction enzymes are shown in lower case.

Primer A: 5' gatccCATGGACATCGACCCTTATAAAGAATTTGG 3'
SEQ ID NO:44

Primer Z, below, is designed to amplify the 3' end of HBcAg and place a TAA stop codon and a HindIII (A'AGCT,T) site following amino acid 183 (Cys).

Primer Z: 5'gatcaAGCTTTTAACATTGAGATTCCCGAGAT

TGAGATCTTCTG 3'

SEQ ID NO:45

A DNA fragment encoding the full-length HBcAg with modified 5' and 3' ends is amplified using plasmid pFS14 DNA as a template in the presence of primer A and primer Z under the standard polymerase chain reaction conditions recommended by the manufacturer of the GeneAmp PCR reagent kit (Perkin Elmer Cetus, Norwalk, Conn.).

The amplified DNA is then cleaved with NcoI and HindIII, and fractionated by size on an agarose gel. Full-length HBcAg DNA is purified from a gel slice using a QIAQUICK™ gel extraction kit (QIAGEN, Chatsworth, CA).

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# B. <u>Insertion Pf HBcAq Onto pProEx1</u>

pProEx1, an E. coli expression vector (Life Technologies, Inc., Gaithersburg, MD), is also cleaved with NcoI and HindIII and gel-purified. The amplified DNA and pProEx1 DNAs are ligated under standard conditions using T4 DNA ligase and transformed into chemically-competent E. coli DH10B cells (Life Technologies, Inc.) using protocols supplied by the vendor to form plasmid ProEx1-AZ. The transformation mixture is spread on LB agar plates containing 100  $\mu$ g/ml ampicillin and incubated overnight at (about 18 hours) at 37°C. Colonies harboring ampicillin-resistant plasmids are purified by restreaking on fresh LB agar plates containing ampicillin, and minipreps of plasmid DNA are prepared using WIZARD™ 373 DNA purification kits (Promega, Inc., Madison, WI). Plasmids containing the HBcAg fragment inserted into the NcoI and HindIII sites of pProEx1 are characterized by restriction mapping and sequence analysis across the inserted region.

Plasmid pProEx1-AZ is then modified to insert a polylinker between the nucleotides that encode amino acid residues 70-75 of HBcAg.

Primer B is designed to insert an XhoI site (C'TCGA) and an EcoRI site (G'AATT,C) site following position 206 of SEQ ID NO:39. Primer Y is designed to insert an EcoRI site (G'AATT,C) site followed by a SpeI site (A'CTAG,T) before position 226 of SEQ ID NO:39.

Primer Y: 5' gatcgAATTCACTAGTTGGAAGATCCAGCGT
CTAGAGACCTAGTAG 3' SEQ ID NO:46

Primer B: 5' gatcgAATTCCTCGAGCTAGAGTCATTAGTT
CCCCCCAGCA 3' SEQ ID NO:47

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Plasmid pProEx1-AZ is then used as a template with primers A and B to amplify a segment of DNA (designated HBcAg-AB) encoding amino acid residues 1-69 of HBcAg to generate a fragment that contains an NcoI site at its 5' end and an XhoI and a EcoRI site at its 3' end. The same plasmid is also used with primers Y and Z to amplify a segment of DNA (designated HBcAg-YZ) encoding amino acid residues 76-183 of HBcAg to generate a fragment that contains EcoRI and SpeI sites at its 5' end and a HindIII site at its 3' end.

The PCR product from the reaction designed to produce plasmid HBcAg-AB is cleaved with NcoI and EcoRI and purified after agarose gel electrophoresis. The PCR product from a second reaction designed to produce plasmid HBcAg-YZ is cleaved with EcoRI and HindIII and purified after agarose gel electrophoresis. The two gel-purified fragments are then ligated in a triple ligation reaction to plasmid pProEx1 that had been treated with NcoI and HindIII and purified after agarose gel electrophoresis. The desired ligated plasmid, pProEx1-AB-YZ, is obtained by screening ampicillin-resistant colonies for plasmids that have the predicted structure by restriction analysis, and is confirmed by DNA sequencing across the whole HBcAg region, particularly the A, BY, and Z junctions.

# C. Cloning Of CETP Segment Encoding SEQ ID NO:29

A stably transformed CHO cell line transfected
with human CETP cDNA [Wang et al., J. Biol. Chem.,
270:612-618 (1995); Wang et al., J. Biol. Chem.,
267:17487-17490 (1992)] provides CETP cDNA that is used
as a template to amplify a segment (nucleotides 1346 to
1431) of the CETP coding sequence (SEQ ID NO: 1) that
encodes the human peptide (SEQ ID NO: 29;
ArgAspGlyPheLeuLeuGlnMetAspPheGlyPheProGluHisLeu

LeuValAspPheLeuGlnSerLeuSer) that is bound by the antibody TP2; T.L. Swenson et al., J. Biol. Chem., 264:14318-14326 (1989).

Primer C, below, is designed to amplify a region from just upstream from the natural XhoI site at position 1346. Primer X, below, is designed to amplify a region at the 3' end of the CETP gene, removing the TAG codon and replacing it with an Eco47III site (AGC|GCT) followed by an EcoRI site (G'AATT,C).

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Primer C: 5' GATTATCACTCGAGATGGCTTCCTGCTGCAG 3' SEQ ID NO:48

Primer X: 5' gatcgAATTCAGCGCTCAAGCTCTGGAGG

AAATCCACCAG 3' SEQ ID NO:49

The CETP cDNA is then used as a template with primers C and X to amplify a segment of DNA (designated pCETP-CX) encoding amino acid residues 461-476 of CETP, that contains an XhoI site near its 5' end and an Eco47III and EcoRI site at its 3' end. This segment, CETP-CX, is then cleaved with XhoI and EcoR47III, and gel-purified. Plasmid pProEx1-AB-YZ is digested with SpeI and treated with T4 DNA polymerase to remove the 4-base 5' overhangs and generate blunt ends. [See, J. Sambrook et al., Molecular Cloning, 2nd 3d., Cold Spring Harbor Press, Cold Spring Harbor N.Y., 8-23 (1989).]

The resulting plasmid is then treated with XhoI, gel-purified, and ligated to the segment CETP-CX that has an XhoI site at one end and a blunt end resulting from cleavage with Eco47III at the other end. The resulting plasmid, designated pProEx1-ABC-XYZ, is characterized by restriction analysis and by sequencing to confirm that it contains sequences encoding amino acid residues 461-476 of CETP replacing sequences that

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encoded amino acid residues 70-75 of HBcAg in the vector pProEx1-AZ.

# Example 4: Expression Of HBcAg/CETP/HBcAg Chimeric Fusion Proteins In E. coli

The pProEx1 vector is designed for the expression of foreign proteins in E. coli. This vector contains a gene conferring resistance to ampicillin and a pBR322 origin of replication for propagation in E. It also has a multiple cloning site flanked by a 6 histidine sequence (6X His) and the recognition sequence for rTEV protease. This site allows for the removal of the 6X His tag from a fusion protein after purification. The vector also has a Trc promoter and lacIq gene permitting inducible gene expression with isopropyl- $\beta$ -D-thiogalactopyranoside (IPTG). procaryotic ribosomal binding site is located upstream from the start of translation of the 6X His tag. unique NcoI site is located at the first codon of the 6X Plasmids pProEx1 and a control plasmid. pProEx1-CAT, are obtained from Life Technologies, Inc.

E. coli DH10B strains individually harboring pProEx1, pProEx1-CAT, pProEx1-AZ, or pProEx1-ABC-XYZ are cultured overnight (about 18 hours), and used as inocula for cultures that are induced with IPTG under conditions recommended by the vendor. Cultures harboring plasmid pProEx1-AZ produce HBcAg and those harboring pProEx1-ABC-XYZ produce the desired HBcAg/CETP/HBcAg fusion protein as particles. These proteins lack the 6X His tag present in the original pProEx1 vector because the HBcAg sequences are inserted at the NcoI site at the beginning of the 6X tag. Cultures harboring pProEx1-CAT produce a protein that migrates on SDS-PAGE gels as expected for a His-tagged CAT fusion protein.

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# Example 5: Expression Of HBcAg/CETP/HBcAg Chimeric Fusion Proteins In Baculovirus-Infected Insect Cells

Baculovirus-infected insect cells have been shown to express a wide variety of recombinant proteins (V.A. Luckow, Insect Cell Expression Technology, pp. 183-218, in Protein Engineering: Principles and Practice, J.L. Cleland et al. eds., Wiley-Liss, Inc, 1996). Heterologous genes placed under the control of the polyhedrin promoter of the Autographa californica nuclear polyhedrosis virus (AcNPV) are often expressed at high levels during the late stages of infection. In most cases, the recombinant proteins are appropriately processed and are functionally similar to their authentic counterparts.

Recombinant baculoviruses containing the chimeric HBcAg/CETP/HBcAg gene are constructed using the baculovirus shuttle vector system (Luckow et al.,  $J.\ Virol.$ , 67:4566-4579, 1993) sold commercially as the Bac-To-Bac<sup>M</sup> baculovirus expression system (Life Technologies, Inc.).

Briefly, pProEx1-ABC-XYZ is digested with NcoI, treated with Klenow enzyme to fill in the ends, and digested with HindIII to release the entire fragment encoding the HBcAg/CETP/HBcAg fusion protein. fragment is inserted into a baculovirus donor plasmid, pFastBac1, that is digested with BamHI, treated with Klenow enzyme, and digested with HindIII. The resulting plasmid has the sequences encoding the hybrid HBcAg/CETP/HBcAg gene inserted downstream from the polyhedrin promoter of AcNPV. The mini-Tn7 segment containing the polyhedrin/HBcAg/CETP/HBcAg expression cassette is then transposed to a baculovirus shuttle vector propagated in E. coli and colonies harboring composite (recombinant) vectors are identified by their color and an altered drug resistance patterns. Miniprep DNAs are prepared and transfected into cultured Spodoptera frugiperda (fall armyworm) Sf9 cells.

Stocks of recombinant viruses are prepared and expression of the recombinant protein is monitored by standard protocols (O'Reilly et al., <u>Baculovirus</u>

<u>Expression Vectors: A Laboratory Manual</u>, W.H. Freeman and Company, New York, 1992; King, L.A., and Possee, R.D. <u>The Baculovirus Expression System: A Laboratory Guide</u>, Chapman & Hall, London, 1992).

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# Example 6: Expression Of HBcAg/CETP/HBcAg Chimeric Fusion Proteins In Mammalian Cells

The HBcAg/CETP/HBcAg fusion protein is expressed in mammalian cell culture using the BHK/VP16 expression system (Hippenmeyer et al., Bio/Technology, 11:1037-1041, 1993). Briefly, the NcoI-HindIII fragment from plasmid pProEx1-ABC-XYZ is isolated by gel electrophoresis and purified as before. The fragment is treated with Klenow polymerase and all four nucleotide triphosphates to make the 5' overhanging ends blunt.

The mammalian expression vector pMON3327 contains the SV40 polyadenylation signal sequence in the BamHI site of plasmid pUC18, and is used as the basis for further plasmid construction. Ligation of the IE175 promoter of herpes simplex virus (HSV-1) upstream of the SV40 polyadenylation signal sequence in vector pMON3327 provides mammalian expression vector pMON3360B. The IE175 promoter is responsive to the HSV-1 VP-16 transactivator.

Expression vector pMON3360B is digested with BamHI and the 5' over hanging ends at the unique BamHI site are filled in using Klenow polymerase. The vector sequences and the HBcAg/CETP/HBcAg sequences are ligated overnight (about 18 hours) at 15°C using T4 DNA ligase. The ligation mixture is transfected into competent E. coli and selected for ampicillin resistance. Plasmid

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DNA is isolated from the colonies and analyzed by restriction analysis for proper orientation of the HBcAg/CETP/HBcAg sequences in the pMON3360B vector. A plasmid with the correct orientation is designated pMON3360B-HBcAg-CETP. Plasmid pMON3360B-HBcAg-CETP is purified using Promega Maxiprep™ protocols from 400 ml cultures.

BHK/VP16 cells are plated at about  $3 \times 10^5$  cells per 60 mm culture dish 24 hours before transfection in growth medium consisting of DMEM/5% fetal bovine sera (Life Technologies). Ten micrograms of plasmid pMON3360B-HBcAg-CETP and 1  $\mu g$  of plasmid pMON1118 are transfected into the cells using LipofectAmine (Life Technologies) as recommended by the manufacturer. Two days after transfection, the cells are treated with trypsin/EDTA (Life Technologies) and plated in ten 100 mm dishes in growth medium containing hygromycin (Sigma). In about two weeks, surviving colonies are isolated using filter paper and expanded and assayed for expression of the HBcAg/CETP/HBcAg fusion protein.

The foregoing description and the examples are intended as illustrative and are not to be taken as limiting. Still other variations within the spirit and scope of this invention are possible and will readily present themselves to those skilled in the art.

#### SEQUENCE LISTING

- (1) GENERAL INFORMATION:
  - (i) APPLICANT: Needleman, Philip Glenn, Kevin Krul, Elaine Gamson, Edward P.
  - (ii) TITLE OF INVENTION: An Immunological Process and Constructs for Increasing the HDL Cholesterol Concentration
  - (iii) NUMBER OF SEQUENCES: 50
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    - (F) ZIP: 60606
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk

    - (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER:(B) FILING DATE:

    - (C) CLASSIFICATION:
  - (viii) ATTORNEY/AGENT INFORMATION:

    - (A) NAME: Gamson, Edward P. (B) REGISTRATION NUMBER: 29,381
    - (C) REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
    - (ix) TELECOMMUNICATION INFORMATION:
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- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1431 base pairs

    - (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (viii) POSITION IN GENOME:
    - (C) UNITS: bp
    - (x) PUBLICATION INFORMATION:
      - (A) AUTHORS: Drayna, Dennis

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McLean, John Henzel, William Kohr, William

Fielding, Christopher

Lawn, Richard

- (B) TITLE: Cloning and sequencing of human cholesteryl ester transfer protein cDNA
- (C) JOURNAL: Nature

(D) VOLUME: 327 (F) PAGES: 632-634 (G) DATE: June 18-1987

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGCTCCAAAG	GCACCTCGCA	CGAGGCAGGC	ATCGTGTGCC	GCATCACCAA	GCCTGCCCTC	60
CTGGTGTTGA	ACCACGAGAC	TGCCAAGGTC	ATCCAGACCG	CCTTCCAGCG	AGCCAGCTAC	120
CCAGATATCA	CGGGCGAGAA	GGCCATGATG	CTCCTTGGCC	AAGTCAAGTA	TGGGTTGCAC	180
AACATCCAGA	TCAGCCACTT	GTCCATCGCC	AGCAGCCAGG	TGGAGCTGGT	GGAAGCCAAG	240
TCCATTGATG	TCTCCATTCA	GAACGTGTCT	GTGGTCTTCA	AGGGGACCCT	GAAGTATGGC	300
TACACCACTG	CCTGGTGGCT	GGGTATTGAT	CAGTCCATTG	ACTTCGAGAT	CGACTCTGCC	360
ATTGACCTCC	AGATCAACAC	ACAGCTGACC	TGTGACTCTG	GTAGAGTGCG	GACCGATGCC	420
CCTGACTGCT	ACCTGTCTTT	CCATAAGCTG	CTCCTGCATC	TCCAAGGGGA	GCGAGAGCCT	480
GGGTGGATCA	AGCAGCTGTT	CACAAATTTC	ATCTCCTTCA	CCCTGAAGCT	GGTCCTGAAG	540
GGACAGATCT	GCAAAGAGAT	CAACGTCATC	TCTAACATCA	TGGCCGATTT	TGTCCAGACA	600
AGGGCTGCCA	GCATCCTTTC	AGATGGAGAC	ATTGGGGTGG	ACATTTCCCT	GACAGGTGAT	660
CCCGTCATCA	CAGCCTCCTA	CCTGGAGTCC	CATCACAAGG	GTCATTTCAT	CTACAAGAAT	720
GTCTCAGAGG	ACCTCCCCCT	CCCCACCTTC	TCGCCCACAC	TGCTGGGGGA	CTCCCGCATG	780
CTGTACTTCT	GGTTCTCTGA	GCGAGTCTTC	CACTCGCTGG	CCAAGGTAGC	TTTCCAGGAT	840
GGCCGCCTCA	TGCTCAGCCT	GATGGGAGAC	GAGTTCAAGG	CAGTGCTGGA	GACCTGGGGC	900
TTCAACACCA	ACCAGGAAAT	CTTCCAAGAG	GTTGTCGGCG	GCTTCCCCAG	CCAGGCCCAA	960
GTCACCGTCC	ACTGCCTCAA	GATGCCCAAG	ATCTCCTGCC	AAAACAAGGG	AGTCGTGGTC	1020
AATTCTTCAG	TGATGGTGAA	ATTCCTCTTT	CCACGCCCAG	ACCAGCAACA	TTCTGTAGCT	1080
TACACATTTG	AAGAGGATAT	CGTGACTACC	GTCCAGGCCT	CCTATTCTAA	GAAAAAGCTC	1140
TTCTTAAGCC	TCTTGGATTT	CCAGATTACA	CCAAAGACTG	TTTCCAACTT	GACTGAGAGC	1200
AGCTCCGAGT	CCATCCAGAG	CTTCCTGCAG	TCAATGATCA	CCGCTGTGGG	CATCCCTGAG	1260
GTCATGTCTC	GGCTCGAGGT	AGTGTTTACA	GCCCTCATGA	ACAGCAAAGG	CGTGAGCCTC	1320
TTCGACATCA	TCAACCCTGA	GATTATCACT	CGAGATGGCT	TCCTGCTGCT	GCAGATGGAC	1380
TTTGGCTTCC	CTGAGCACCT	GCTGGTGGAT	TTCCTCCAGA	GCTTGAGCTA	G	1431

### (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 amino acids
   (B) TYPE: amino acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln Ala Gln

Val Ala Val His

- (2) INFORMATION FOR SEQ ID NO:3:
  - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 amino acids

    - (B) TYPE: amino acid (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Ala Val Thr Phe Arg Phe Pro Arg Pro Asp Gly Arg Glu Ala Val

Ala Tyr Arg Phe 20

- (2) INFORMATION FOR SEQ ID NO:4:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 22 amino acids(B) TYPE: amino acid

    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Leu Gln Met Asp Phe Gly Phe Pro Lys His Leu Leu Val Asp

Phe Leu Gln Ser Leu Ser 20

- (2) INFORMATION FOR SEQ ID NO:5:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu His Leu

Leu Asp Phe Gln

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Leu His Leu Gln Gly Glu Arg Glu Pro Gly Trp Leu Lys Gln 10

Leu Phe Thr Asn

- (2) INFORMATION FOR SEQ ID NO:7:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids (B) TYPE: amino acid

    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Leu His Asn 20

- (2) INFORMATION FOR SEQ ID NO:8:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln 10

Val Thr Val His

- (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids(B) TYPE: amino acid(C) STRANDEDNESS: single

    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Met Val Lys Phe Leu Phe Pro Arg Pro Asp Gln Gln His Ser Val

Ala Tyr Thr Phe

- (2) INFORMATION FOR SEQ ID NO:10:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 22 amino acids (B) TYPE: amino acid

    - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide

  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu Val Asp

Phe Leu Gln Ser Leu Ser 20

- (2) INFORMATION FOR SEQ ID NO:11:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids (B) TYPE: amino acid

    - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide

  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Leu Phe Leu Ser Leu

Leu Asp Phe Gln 20

- (2) INFORMATION FOR SEQ ID NO:12:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Leu His Leu Gln Gly Glu Arg Glu Pro Gly Trp Ile Lys Gln

Leu Phe Thr Asn 20

- (2) INFORMATION FOR SEQ ID NO:13:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids (B) TYPE: amino acid

    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Ile Thr Gly Glu Lys Ala Met Met Leu Leu Gly Gln Val Lys Tyr

Gly Leu His Asn

- (2) INFORMATION FOR SEQ ID NO:14:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 63 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: single
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (viii) POSITION IN GENOME: (C) UNITS: bp
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAGGAAATCT TCCAGGAGCT TTCCAGAGGC CTTCCCACCG GCCAGGCCCA GGTAGCCGTC

CAC

60

60

- (2) INFORMATION FOR SEQ ID NO:15:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 60 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (viii) POSITION IN GENOME:
    - (C) UNITS: bp
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTCGCCGTGA CGTTCCGCTT CCCCCGCCCA GATGGCCGAG AAGCTGTGGC CTACAGGTTT

- (2) INFORMATION FOR SEQ ID NO:16:
  - (i) SEQUENCE CHARACTERISTICS:

<ul><li>(A) LENGTH: 66 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: DNA (genomic)	
(viii) POSITION IN GENOME: (C) UNITS: bp	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
CTGCTGCTGC AGATGGACTT CGGTTTTCCC AAGCACCTGC TGGTGGATT	r cctgcagagc 60
CTGAGC	66
(2) INFORMATION FOR SEQ ID NO:17:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 60 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(viii) POSITION IN GENOME: (C) UNITS: bp	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
ACCACCGTCC AGGCCTCCTA CTCCCAGAAA AAGCTCTTCC TACACCTCT	T GGATTTCCAG 60
(2) INFORMATION FOR SEQ ID NO:18:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 60 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(viii) POSITION IN GENOME: (C) UNITS: bp	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
CTGCTCCTGC ACCTCCAGGG GGAGCGCGAG CCGGGGTGGC TCAAGCAGC	T CTTCACAAAC 60
(2) INFORMATION FOR SEQ ID NO:19:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 60 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: DNA (genomic)	

(viii) POSITION IN GENOME:

(viii) POSITION IN GENOME: (C) UNITS: bp

(C) UNITS: bp	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
GACGTCAGCG GCGAGAGGGC CGTGATGCTC CTCGGCCGGG TCAAGTACGG GCTGCACA	AC 60
(2) INFORMATION FOR SEQ ID NO:20:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 63 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: DNA (genomic)	
(viii) POSITION IN GENOME: (C) UNITS: bp	,
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
CAGGAAATCT TCCAAGAGGT TGTCGGCGGC TTCCCCAGCC AGGCCCAAGT CACCGTCC	CAC 60
TGC	63
(2) INFORMATION FOR SEQ ID NO:21:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 60 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: DNA (genomic)	
(viii) POSITION IN GENOME: (C) UNITS: bp	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
GTGATGGTGA AATTCCTCTT TCCACGCCCA GACCAGCAAC ATTCTGTAGC TTACACAT	TTT 60
(2) INFORMATION FOR SEQ ID NO:22:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 66 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: DNA (genomic)	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
CTGCTGCTGC AGATGGACTT TGGCTTCCCT GAGCACCTGC TGGTGGATTT CCTCCAGAGC
TTGAGC 6
(2) INFORMATION FOR SEQ ID NO:23:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 60 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(viii) POSITION IN GENOME: (C) UNITS: bp
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
ACTACCGTCC AGGCCTCCTA TTCTAAGAAA AAGCTCTTCT TAAGCCTCTT GGATTTCCAG
(2) INFORMATION FOR SEQ ID NO:24:
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 60 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>
(ii) MOLECULE TYPE: DNA (genomic)
(viii) POSITION IN GENOME: (C) UNITS: bp
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
CTGCTCCTGC ATCTCCAAGG GGAGCGAGAG CCTGGGTGGA TCAAGCAGCT GTTCACAAAT 6
(2) INFORMATION FOR SEQ ID NO:25:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 60 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(viii) POSITION IN GENOME: (C) UNITS: bp
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
GATATCACGG GCGAGAAGGC CATGATGCTC CTTGGCCAAG TCAAGTATGG GTTGCACAAC 6
(2) INFORMATION FOR SEC ID NO.26.

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 497 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (x) PUBLICATION INFORMATION:
  - (A) AUTHORS: Nagashima, M. McLean, J. W. Lawn, R. M.
  - (B) TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protein
  - (C) JOURNAL: J. Lipid Res.
  - (D) VOLUME: 29
  - (F) PAGES: 1643-1649 (G) DATE: 1988
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
- Ala Cys Pro Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys Arg Ile 1 5 10 15
- Thr Lys Pro Ala Leu Leu Val Leu Asn Gln Glu Thr Ala Lys Val Val
- Gln Thr Ala Phe Gln Arg Ala Gly Tyr Pro Asp Val Ser Gly Glu Arg
- Ala Val Met Leu Leu Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln 50 60
- Ile Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp Ala
- Lys Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val Val Phe Lys Gly
- Thr Leu Asn Tyr Ser Tyr Thr Ser Ala Trp Gly Leu Gly Ile Asn Gln
- Ser Val Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr
- Glu Leu Thr Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys
- Tyr Leu Ala Phe His Lys Leu Leu His Leu Gln Gly Glu Arg Glu 145 150 150 155
- Pro Gly Trp Leu Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu
- Lys Leu Ile Leu Lys Arg Gln Val Cys Asn Glu Ile Asn Thr Ile Ser
- Asn Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser 200
- Asp Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro Val Ile 210 220
- Thr Ala Thr Tyr Leu Glu Ser His His Lys Gly His Phe Thr His Lys
- Asn Val Ser Glu Ala Phe Pro Leu Arg Ala Phe Pro Pro Gly Leu Leu

Gly Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn

Ser Leu Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser Leu

Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln Gly Phe Asp Thr

Asn Gln Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln 310

Ala Gln Val Ala Val His Cys Leu Lys Val Pro Lys Ile Ser Cys Gln

Asn Arg Gly Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe

Pro Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp

Ile Ile Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu

His Leu Leu Asp Phe Gln Cys Val Pro Ala Ser Gly Arg Ala Gly Ser 390

Ser Ala Asn Leu Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser

Asn Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu Arg Ser

Leu Ile Ala Thr Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val

Ala Phe Thr Ala Leu Met Asn Ser Lys Gly Leu Asp Leu Phe Glu Ile 455

Ile Asn Pro Glu Ile Ile Thr Leu Asp Gly Cys Leu Leu Gln Met 465 470 475 480

Asp Phe Gly Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser Leu 485

Ser

#### (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1494 base pairs (B) TYPE: nucleic acid

  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

# (viii) POSITION IN GENOME:

(C) UNITS: bp

#### (x) PUBLICATION INFORMATION:

- (A) AUTHORS: Nagashima, Mariko McLean, John W.
- Lawn, Richard M.
  (B) TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protein (C) JOURNAL: J. Lipid Res.

(D) VOLUME: 29 (F) PAGES: 1643-1649 (G) DATE: 1988

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

60	CAAGCCCGCC	GTCGCATCAC	GGCATCGTGT	CTACGAGGCT	AAGGCGCCTC	GCCTGTCCCA
120	GCGCGCCGGC	CGGCCTTCCA	GTGGTCCAGA	GACGGCCAAG	TGAACCAAGA	CTCTTGGTGT
180	GTACGGGCTG	GCCGGGTCAA	ATGCTCCTCG	GAGGGCCGTG	TCAGCGGCGA	TATCCGGACG
240	GGTGGACGCC	AGGTGGAGCT	GCCAGCAGCC	CCTGTCCATC	AGATCAGCCA	CACAACCTCC
300	CCTGAACTAC	TCAAGGGGAC	TCCGTGGTCT	CCAGAACGTG	ACGTCGCCAT	AAGACCATCG
360	GATCGACTCT	TCGACTTCGA	AATCAGTCTG	GTTGGGCATC	GTGCCTGGGG	AGCTACACGA
420	GCGCACCAAT	CTGGCAGTGT	ACCTGCGACG	CACAGAGCTG	TCCAGATCAA	GCCATTGACC
480	GGAGCGCGAG	ACCTCCAGGG	CTGCTCCTGC	TTTCCATAAA	GCTACCTGGC	GCCCCGACT
540	GCTGATTCTG	TCACCCTGAA	TTCATCTCCT	CTTCACAAAC	TCAAGCAGCT	CCGGGGTGGC
600	CTTTGTCCAG	TCATGGCTGA	ATCTCCAACA	GATCAACACC	TCTGCAATGA	AAGCGACAGG
660	CGTGACGGGG	TGGACATTTC	GACATCGGGG	CTCAGATGGA	CCAGCATCCT	ACGAGGGCCG
720	CACGCACAAG	AGGGTCACTT	TCCCATCACA	CTACCTGGAG	TCACAGCCAC	GCCCCTGTCA
780	GGACTCCCGC	GTCTTCTGGG	TTCCCGCCCG	CCTCCGCGCC	AGGCCTTCCC	AACGTCTCCG
840	CGCCTTCCAG	TGGCCAGGGC	CTCAACTCCC	CGATCAAGTG	TCTGGTTCTC	ATGCTCTACT
900	GGAGACCCAG	AGAAAGTGCT	GATGAGTTCA	CCTGACAGGG	TCGTGCTCAG	GAGGGCCGTC
960	CACCGGCCAG	GAGGCCTTCC	GAGCTTTCCA	AATCTTCCAG	CCAACCAGGA	GGTTTCGACA
1020	CCGGGGTGTC	CCTGCCAGAA	CCCAAGATCT	CCTTAAGGTG	CCGTCCACTG	GCCCAGGTAG
1080	CCGAGAAGCT	GCCCAGATGG	CGCTTCCCCC	CGTGACGTTC	CTTCCGTCGC	GTGGTGTCTT
1140	CTCCCAGAAA	AGGCCTCCTA	ACCACCGTCC	GGATATCATC	GGTTTGAGGA	GTGGCCTACA
1200	GGCAGGCAGC	CCAGCGGAAG	TGCGTGCCGG	GGATTTCCAG	TACACCTCTT	AAGCTCTTCC
1260	CCTGACTGAG	CTGTTTCCAA	GAGGCTAAGG	CCTCAGGACT	TCTCCGTGGC	TCAGCAAATC
1320	GGGCATCCCG	TCGCCACGGT	CGCTCCCTGA	GAGCTCTCTC	AGTCCCTGCA	AGCCGCTCCG
1380	AGGCCTGGAC	TGAACAGCAA	ACAGCCCTCA	GGTGGCGTTC	CTCGGCTCGA	GAGGTCATGT
1440	GCTGCAGATG	GCTGCCTGCT	ACTCTCGATG	CGAGATTATC	TCATCAACCC	CTCTTCGAAA
1494	CTAG	AGAGCCTGAG	GATTTCCTGC	CCTGCTGGTG	TTCCCAAGCA	GACTTCGGTT

# (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 476 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

 $(\mathbf{x})$  PUBLICATION INFORMATION:

(A) AUTHORS: Drayna, Dennis

Jarnagin, Alisha Stephens

McLean, John Henzel, William Kohr, William

Fielding, Christopher

Lawn, Richard

- (B) TITLE: Cloning and sequencing of human cholesteryl ester transfer protein cDNA
- (C) JOURNAL: Nature
- (D) VOLUME: 327
- (F) PAGES: 632-634
- (G) DATE: June 18-1987

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val Cys Arg Ile Thr 1  $\phantom{-}$  15

Lys Pro Ala Leu Leu Val Leu Asn His Glu Thr Ala Lys Val Ile Gln
20 25 30

Thr Ala Phe Gln Arg Ala Ser Tyr Pro Asp Ile Thr Gly Glu Lys Ala 35 40 45

Met Met Leu Leu Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln Ile 50 55 60

Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Glu Ala Lys 65 70 75 80

Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val Val Phe Lys Gly Thr 85  $\phantom{-}90\phantom{00}$ 

Leu Lys Tyr Gly Tyr Thr Thr Ala Trp Trp Leu Gly Ile Asp Gln Ser 100 105 110

Ile Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Gln 115 120 125

Leu Thr Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys Tyr 130 135 140

Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro 145 150 155 160

Gly Trp Ile Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu Lys

Leu Val Leu Lys Gly Gln Ile Cys Lys Glu Ile Asn Val Ile Ser Asn 180 185 190

Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp 195 200 205

Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro Val Ile Thr 210 220

Ala Ser Tyr Leu Glu Ser His His Lys Gly His Phe Ile Tyr Lys Asn 225 230 235 240

Val Ser Glu Asp Leu Pro Leu Pro Thr Phe Ser Pro Thr Leu Leu Gly
245 250 255

Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Glu Arg Val Phe His Ser 260 265 270

Leu Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met Leu Ser Leu Met 275 280 285

- Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp Gly Phe Asn Thr Asn 295 300
- Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln 310
- Val Thr Val His Cys Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys
- Gly Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro Arg
- Pro Asp Gln Gln His Ser Val Ala Tyr Tyr Phe Glu Glu Asp Ile Val
- Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Leu Phe Leu Ser Leu
- Leu Asp Phe Gln Ile Thr Pro Lys Thr Val Ser Asn Leu Thr Glu Ser
- Ser Ser Glu Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val
- Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val Phe Thr Ala Leu
- Met Asn Ser Lys Gly Val Ser Leu Phe Asp Ile Ile Asn Pro Glu Ile
- Ile Thr Arg Asp Gly Phe Leu Leu Leu Gln Met Asp Phe Gly Phe Pro
- Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
- (2) INFORMATION FOR SEQ ID NO:29:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 26 amino acids

    - (B) TYPE: amino acid (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (x) PUBLICATION INFORMATION:
    - (A) AUTHORS: Swenson, T. L. et al.,
    - (C) JOURNAL: J. Biol. Chem. (D) VOLUME: 264
    - (F) PAGES: 14318-14326 (G) DATE: 1989
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
  - Arg Asp Gly Phe Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His
  - Leu Leu Val Asp Phe Leu Gln Ser Leu Ser 20
- (2) INFORMATION FOR SEQ ID NO:30:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 493 amino acids (B) TYPE: amino acid

    - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (x) PUBLICATION INFORMATION:
  - (A) AUTHORS: Pape, Michael E. Rehberg, Edward F. Marotti, Keith R.
  - of Cynomolgus Monkey Cholesteryl Ester Transfer Protein
  - (C) JOURNAL: Arteriosclerosis and Thrombosis
  - (D) VOLUME: 11

  - (E) ISSUE: 6 (F) PAGES: 1759-1771
  - (G) DATE: Nov/Dec-1991
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
- Met Leu Ala Ala Thr Val Leu Thr Leu Ala Leu Leu Gly Asn Val His
- Ala Cys Ser Lys Gly Thr Ser His Lys Ala Gly Ile Val Cys Arg Ile 20 25 30
- Thr Lys Pro Ala Leu Leu Val Leu Asn Gln Glu Thr Ala Lys Val Ile 35 40 45
- Gln Ser Ala Phe Gln Arg Ala Asn Tyr Pro Asn Ile Thr Gly Glu Lys
- Ala Met Met Leu Leu Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln 65 70 75 80
- Ile Ser His Leu Ser Ile Ala Ser Ser Arg Val Glu Leu Val Glu Ala
- Lys Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val Val Phe Lys Gly
- Thr Leu Lys Tyr Gly Tyr Thr Thr Ala Trp Gly Leu Gly Ile Asp Gln
- Gln Leu Thr Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys
- Tyr Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu
- Pro Gly Trp Ile Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu
- Lys Leu Val Leu Lys Gly Gln Ile Cys Lys Glu Ile Asn Ile Ile Ser
- Asn Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser
- Asp Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro Ile Ile
- Thr Ala Ser Tyr Leu Glu Ser His His Lys Gly Tyr Phe Ile Tyr Lys

- Asn Val Ser Glu Asp Leu Pro Leu Pro Thr Phe Ser Pro Ala Leu Leu 260 265 270
- Gly Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Glu Gln Val Phe His 275 280 285
- Ser Leu Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Thr Leu Ser Leu 290 295 300
- Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp Gly Phe Asn Thr 305 310 315 320
- Asn Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala 325 330 335
- Gln Val Thr Val His Cys Leu Lys Met Pro Arg Ile Ser Cys Gln Asn 340 345 350
- Lys Gly Val Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro 355 360 365
- Arg Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu Glu Asp Ile 370 375 380
- Met Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Leu Phe Leu Ser 385 390 395 400
- Leu Leu Asp Phe Gln Ile Thr Pro Lys Thr Val Ser Asn Leu Thr Glu 405 410 415
- Ser Ser Ser Glu Ser Val Gln Ser Phe Leu Gln Ser Met Ile Thr Thr 420 425 430
- Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Ala Val Phe Thr Ala 435 440 445
- Leu Met Asn Ser Lys Gly Leu Ser Leu Phe Asp Ile Ile Asn Pro Glu 450 455 460
- Ile Ile Thr Arg Asp Gly Phe Leu Leu Gln Met Asp Phe Gly Phe 465 470 475 480
- Pro Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser 485
- (2) INFORMATION FOR SEQ ID NO:31:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1508 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (x) PUBLICATION INFORMATION:
    - (A) AUTHORS: Pape, Michael E.
      Rehberg, Edward F.
      Marotti, Keith R.
      Melchior, George M
    - Melchior, George W.

      (B) TITLE: Molecular Cloning, Sequence, and Expression of Cynomolgus Monkey Cholesteryl Ester Transfer Protein
    - (C) JOURNAL: Arteriosclerosis and Thrombosis
    - (D) VOLUME: 11
    - (E) ISSUE: 6
    - (F) PAGES: 1759-1771
    - (G) DATE: Nov/Dec-1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

#### ATGCTGGCTG CCACCGTCCT GACCCTGGCC CTGCTGGGCA ATGTCCACGC CTGCTCCAAA 60 GGTACCTCAC ACAAGGCAGG CATTGTGTGC CGCATCACCA AGCCTGCCCT CCTGGTGTTG 120 AACCAACAGA CTGCCAAGGT GATCCAGTCT GCCTTCCAGC GAGCCAACTA CCCAAATATC 180 240 ATCAGCCACT TGTCCATCGC CAGCAGCCGG GTGGAGCTGG TGGAAGCCAA GTCCATTGAT 300 GTCTCCATTC AGAACGTGTC TGTGGTCTTC AAGGGGACCC TGAAGTATGG CTACACCACT 360 GCCTGGGGGC TGGGCATTGA TCAGTCCGTT GACTTCGAGA TCGACTCTGC CATTGACCTC 420 CAGATCAACA CACAACTGAC CTGTGACTCT GGTAGAGTGA GGACTGATGC CCCTGACTGC 480 TACCTGTCTT TCCATAAGCT GCTCCTGCAT CTCCAAGGGG AGCGAGAGCC CGGGTGGATC 540 AAGCAGCTGT TCACAAACTT CATCTCCTTC ACCCTGAAGC TGGTCCTGAA GGGACAGATC 600 TGCAAAGAGA TCAACATCAT CTCCAACATC ATGGCCGATT TTGTCCAGAC AAGGGCTGCC 660 AGTATCCTTT CAGATGGAGA CATCGGGGTG GACATTTCCC TGACAGGTGA TCCCATCATT 720 ACAGCCTCCT ACCTGGAGTC CCATCACAAG GGTTATTTCA TCTATAAGAA TGTCTCGGAG 780 GACCTCCCAC TCCCCACCTT CTCGCCCGCA CTGCTGGGGG ACTCCCGCAT GCTGTACTTC 840 TGGTTCTCCG AGCAAGTCTT CCACTCCTG GCCAAGGTAG CTTTCCAAGA TGCCCGCCTC 900 ACGCTCAGCC TGATGGGAGA CGAGTTCAAG GCAGTGCTGG AGACCTGGGG CTTCAACACC 960 AACCAAGAAA TCTTCCAGGA GGTTGTCGGC GGCTTCCCCA GCCAGGCCCA AGTCACCGTC 1020 CACTGCCTCA AGATGCCCAG GATCTCCTGC CAAAACAAGG GAGTCGTGGT CAATTCTTCG 1080 GTGATGGTGA AATTCCTCTT TCCACGCCCA GACCAGCAAC ACTCTGTAGC TTACACATTT 1140 GAAGAGGATA TCATGACCAC CGTCCAGGCC TCCTATTCTA AGAAAAAGCT CTTCTTAAGC 1200 CTCTTGGATT TCCAGATTAC ACCAAAGACT GTTTCCAACT TGACTGAGAG CAGCTCCGAG 1260 TCCGTCCAGA GCTTCCTGCA GTCAATGATC ACCACTGTGG GCATCCCTGA GGTCATGTCT 1320

CGGCTTGAGG CAGTGTTTAC AGCCCTCATG AACAGCAAAG GCCTGAGCCT CTTCGACATC

ATCAATCCTG AGATTATCAC TCGAGATGGC TTCCTGCTGC TGCAGATGGA CTTTGGCTTC

CCTGAGCACC TGCTGGTGGA TTTCCTCCAG AGCTTGAGCT AGAAGTCTCC AAGGACGTCA

1380

1440

1500

1508

## (2) INFORMATION FOR SEQ ID NO:32:

GGATGGGG

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln

Val Thr Val His

- (2) INFORMATION FOR SEQ ID NO:33:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids

    - (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val Met Val Lys Phe Leu Phe Pro Arg Pro Asp Gln Gln His Ser Val

Ala Tyr Thr Phe 20

- (2) INFORMATION FOR SEQ ID NO:34:
  - (i) SEQUENCE CHARACTERISTICS:

    - (A) LENGTH: 22 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: peptide
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu Val Asp

Phe Leu Gln Ser Leu Ser 20

- (2) INFORMATION FOR SEQ ID NO:35:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids (B) TYPE: amino acid

    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Leu Phe Leu Ser Leu

Leu Asp Phe Gln

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Leu Leu His Leu Gln Gly Glu Arg Glu Pro Gly Trp Ile Lys Gln

Leu Phe Thr Asn 20

- (2) INFORMATION FOR SEQ ID NO:37:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Asn Ile Thr Gly Glu Lys Ala Met Met Leu Leu Gly Gln Val Lys Tyr 1 5 10 15

Gly Leu His Asn 20

- (2) INFORMATION FOR SEQ ID NO:38:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 183 amino acids (B) TYPE: amino acid

    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala

Ser	Arg	Asp	Leu	Val 85	Val	Ser	Tyr	Val	Asn 90	Thr	Asn	Met	Gly	Leu 95	Lys
Phe	Arg	Gln	Leu 100	Leu	Trp	Phe	His		Ser			Thr	Phe 110	Gly	Arg
Glu	Thr	Val 115	Ile	Glu	Tyr	Leu	Val 120	Ser	Phe	Gly	Val	Trp 125	Ile	Arg	Thi
Pro	Pro 130	Ala	Tyr	Arg	Pro	Pro 135	Asn	Ala	Pro	Ile	Leu 140	Ser	Thr	Leu	Pro
Glu 145	Thr	Thr	Val	Val	Arg 150	Arg	Arg	Gly	Arg			Arg			Th:
Pro	Ser								Ser						

Gln Ser Arg Glu Ser Gln Cys 180

- (2) INFORMATION FOR SEQ ID NO:39:
  - (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 552 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATGGACATCG	ACCCTTATAA	AGAATTTGGA	GCTACTGTGG	AGTTACTCTC	GTTTTTGCCT	60
TCTGACTTCT	TTCCTTCAGT	ACGAGATCTT	CTAGATACCG	CCTCAGCTCT	GTATCGGGAA	120
GCCTTAGAGT	CTCCTGAGCA	TTGTTCACCT	CACCATACTG	CACTCAGGCA	AGCAATTCTT	180
TGCTGGGGGG	AACTAATGAC	TCTAGCTACC	TGGGTGGGTG	TTAATTTGGA	AGATCCAGCG	240
TCTAGAGACC	TAGTAGTCAG	TTATGTCAAC	ACTAATATGG	GCCTAAAGTT	CAGGCAACTC	300
TTGTGGTTTC	ACATTTCTTG	TCTCACTTTT	GGAAGAGAAA	CAGTTATAGA	GTATTTGGTG	360
TCTTTCGGAG	TGTGGATTCG	CACTCCTCCA	GCTTATAGAC	CACCAAATGC	CCCTATCCTA	420
TCAACACTTC	CGGAGACTAC	TGTTGTTAGA	CGACGAGGCA	GGTCCCCTAG	AAGAAGAACT	480
CCCTCGCCTC	GCAGACGAAG	GTCTCAATCG	CCGCGTCGCA	GAAGATCTCA	ATCTCGGGAA	540
TCTCAATGTT	AG					552

- (2) INFORMATION FOR SEQ ID NO:40:
  - (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 25 amino acids
     (B) TYPE: amino acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu Val

Val Ser Tyr Val Asn Thr Asn Met Gly

- (2) INFORMATION FOR SEQ ID NO:41:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 21 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val

Ile Glu Tyr Leu Val 20

- (2) INFORMATION FOR SEQ ID NO:42:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 16 amino acids (B) TYPE: amino acid

    - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln Leu

- (2) INFORMATION FOR SEQ ID NO:43:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 21 amino acids
      (B) TYPE: amino acid

    - (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro 10

Asn Ala Pro Ile Leu

(2) INFORMATION FOR SEQ ID NO:44:

(i	) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 35 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii	) MOLECULE TYPE: cDNA	
(xi	) SEQUENCE DESCRIPTION: SEQ ID NO:44:	
GATCCCA	TGG ACATCGACCC TTATAAAGAA TTTGG	35
(2) INF	ORMATION FOR SEQ ID NO:45:	
(i	) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 44 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii	) MOLECULE TYPE: cDNA	
(xi	) SEQUENCE DESCRIPTION: SEQ ID NO:45:	
	CTT TTAACATTGA GATTCCCGAG ATTGAGATCT TCTG	
	ORMATION FOR SEQ ID NO:46:	44
(1	) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 43 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii	) MOLECULE TYPE: cDNA	
(	A GEOVERNOLE DESCRIPTION AND TRANSPORTED TO	
	) SEQUENCE DESCRIPTION: SEQ ID NO:46:	
	TTC ACTAGTTGGA AGATCCAGCG TCTAGAGACC TAG	43
	ORMATION FOR SEQ ID NO:47:	
(i	) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii	) MOLECULE TYPE: cDNA	
	) SEQUENCE DESCRIPTION: SEQ ID NO:47:	
GATCGAA'	TTC CTCGAGCTAG AGTCATTAGT TCCCCCCAGC A	41
(2) INF	ORMATION FOR SEQ ID NO:48:	
(i	) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs	

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

	(ii)	MOLE	CUL	E TY:	PE: o	DNA											
	(	anon			a an T 1	>===											
		SEQU								:48:							
		CT CG							G								34
(2)	INFO	RMATI	ON 1	FOR :	SEQ :	ID NO	0:49	:									
	(i)	(B) (C)	LEI TYI STI	NGTH PE: 1 RANDI	ARACT : 40 nucle EDNES	base eic a SS: s	e pa: acid sing:	irs									
	(ii)	MOLE	CULI	TY:	PE: o	DNA										*	
	(xi)	SEQU	ENC	E DES	SCRII	PTIO	N: S	EQ II	ои с	:49:							
GATC	GAAT'	rc ag	CGC:	CAA	G CTC	CTGG	AGGA	AAT	CCAC	CAG							40
(2)	INFO	RMATI	ON I	FOR S	SEQ I	D N	0:50	:									
	(i)	(B) (C)	LEI TYI STI	IGTH PE: 8 RANDI	ARACT : 26 amino EDNES	amin ac: SS: 8	no ao id sing:	cids									
	(ii)	MOLE	CULI	TYI	PE: p	ept:	i.de										
	(253)	SEQU	ENICI	ייבורו יי	י א מי אי	) TT T ( )	a. Ci	70 TI	> NT/>								
								~									
	Leu 1	Asp	Gly	Cys	Leu 5	Leu	Leu	Gln	Met	Asp 10	Phe	Gly	Phe	Pro	Lys 15	His	
	Leu	Leu	Val	Asp 20	Phe	Leu	Gln	Ser	Leu 25	Ser							

## Claims

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1. A process for increasing the concentration of HDL cholesterol in the blood of a mammal whose blood contains cholesteryl ester transfer protein (CETP) that comprises the steps of:

(a) immunizing said mammal with an inoculum containing a CETP immunogen that is dissolved or dispersed in a vehicle, said CETP immunogen comprising an immunogenic polypeptide covalently bonded to an exogenous antigenic carrier polypeptide that is selected from the group consisting of hepatitis B core protein, tetanus toxoid, tuberculin purified protein derivative, diphtheria toxoid and branched oligolysine, said immunogenic polypeptide having a CETP amino acid residue sequence; and

(b) maintaining said immunized mammal for a time period sufficient for said immunogenic polypeptide to induce the production of antibodies that bind to CETP and lessen the transfer of cholesteryl esters from HDL.

- 2. The process according to claim 1 wherein said immunogenic polypeptide is recombinant human CETP.
- 3. The process according to claim 1 wherein said CETP immunogen comprises a fusion protein in which said exogenous antigenic carrier is peptide-bonded to the amino-terminus, carboxy-terminus or both of said immunogenic polypeptide.

4. The process according to claim 3 wherein the carboxy-terminus of said exogenous antigenic carrier is peptide-bonded to the amino-terminus of said immunogenic polypeptide.

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5. The process according to claim 3 wherein said exogenous antigenic carrier is peptide-bonded to both the amino-terminus and carboxy-terminus of said immunogenic polypeptide.

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- 6. The process according to claim 5 wherein said fusion protein is comprised of an immunogenic polypeptide having a length of about 10 to about 30 amino acid residues that is peptide-bonded to an aminoterminal flanking sequence and a carboxy-terminal flanking sequence, wherein
- (a) said amino-terminal flanking sequence consists essentially of about 10 to about 20 amino acid residues having an amino acid residue sequence of the hepatitis B core protein (HBcAg) from about position 1 to about position 35, and said carboxy-terminal sequence consists essentially of about 120 to about 160 amino acid residues having an amino acid residue sequence of HBcAg from about position 10 about position 183, or
- (b) said amino-terminal flanking sequence consists essentially of about 70 to about 90 residues having the amino acid residue sequence of HBcAg from about position 1 to about position 90, and said carboxy-terminal flanking sequence consists essentially of about 65 to about 85 amino acid residues having the amino acid residue sequence of HBcAg from about position 80 to about position 183.
- 7. The process according to claim 6 wherein the number of amino acid residues present in said immunogenic polypeptide is about equal in number to the number of amino acid residues absent from said HBcAg amino acid residue sequence between the carboxy-terminal residue position of said amino-terminal flanking

sequence and the amino-terminal residue of said carboxyterminal flanking sequence.

- 8. The process according to claim 6 wherein said fusion protein is present in said vehicle as particles.
- 9. The process according to claim 1 wherein said immunizing step is repeated.

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- 10. The process according to claim 9 wherein said immunizing step is repeated at intervals of about 3 to about 6 months until the HDL cholesterol value in the blood of said mammal is increased by about 10 percent or more relative to the HDL cholesterol value prior to said first immunization step.
- 11. A process for increasing the concentration of HDL cholesterol in the blood of a mammal whose blood contains cholesteryl ester transfer protein (CETP) that comprises the steps of:
- (a) immunizing said mammal with an inoculum containing a vehicle in which is dissolved or dispersed a CETP immunogen that is a fusion protein of (i) an exogenous antigenic carrier polypeptide that is peptide-bonded to the amino-terminus, carboxy-terminus or both of (ii) an immunogenic polypeptide having a CETP amino acid residue sequence;
- (b) maintaining said mammal for a time period sufficient for said immunogenic polypeptide to induce the production of antibodies that bind to CETP and lesson the transfer of cholesteryl esters from HDL; and
- (c) repeating said immunizing step until the HDL cholesterol value in the blood of said mammal is

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increased by about 10 percent or more relative to the HDL cholesterol value prior to said first immunization step.

- 5 12. The process according to claim 11 wherein said immunogenic polypeptide is human CETP.
  - 13. The process according to claim 12 wherein said exogenous antigenic carrier polypeptide is peptide-bonded to the amino-terminus of said human CETP.
  - 14. The process according to claim 11 wherein said fusion protein is comprised of an immunogenic polypeptide having a length of about 10 to about 30 amino acid residues that is peptide-bonded to an aminoterminal flanking sequence and a carboxy-terminal flanking sequence, wherein
  - (a) said amino-terminal flanking sequence consists essentially of about 10 to about 20 amino acid residues having an amino acid residue sequence of the hepatitis B core protein (HBcAg) from about position 1 to about position 35, and said carboxy-terminal sequence consists essentially of about 120 to about 160 amino acid residues having an amino acid residue sequence of HBcAg from about position 10 about position 183, or
  - (b) said amino-terminal flanking sequence consists essentially of about 70 to about 90 residues having the amino acid residue sequence of HBcAg from about position 1 to about position 90, and said carboxy-terminal flanking sequence consists essentially of about 65 to about 85 amino acid residues having the amino acid residue sequence of HBcAg from about position 80 to about position 183.

15. The process according to claim 14 wherein said immunogenic polypeptide has the sequence of the carboxy-terminal 30 amino acid residues of human CETP and includes the polypeptide of SEQ ID NO:10.

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- 16. The process according to claim 15 wherein said fusion protein consists essentially of a polypeptide of SEQ ID NO:38 from amino acid residue position 1 through position 69, SEQ ID NO:29 and SEQ ID NO:38 from amino acid residue position 76 through position 183 peptide-bonded to each other in the order recited from amino-terminus to carboxy-terminus.
- 17. The process according to claim 16 wherein said fusion protein is present in said vehicle as particles.
  - 18. A cholesteryl ester transfer protein (CETP) immunogen that comprises a fusion protein in which an immunogenic polypeptide having a CETP amino acid residue sequence is covalently bonded to an exogenous antigenic carrier.
  - 19. The immunogen according to claim 18 wherein said exogenous antigenic carrier is peptide-bonded to the amino-terminus, carboxy-terminus or both of said immunogenic polypeptide.
  - 20. The immunogen according to claim 19 wherein the carboxy-terminus of said exogenous antigenic carrier is peptide-bonded to the amino-terminus of said immunogenic polypeptide.
- 21. The process according to claim 20 wherein said exogenous antigenic carrier is peptide-bonded to

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both the amino-terminus and carboxy-terminus of said immunogenic polypeptide.

22. The immunogen according to claim 21 wherein said fusion protein is comprised of an immunogenic polypeptide having a length of about 10 to about 30 amino acid residues that is peptide-bonded to an amino-terminal flanking sequence and a carboxyterminal flanking sequence, wherein

(a) said amino-terminal flanking sequence consists essentially of about 10 to about 20 amino acid residues having an amino acid residue sequence of the hepatitis B core protein (HBcAg) from about position 1 to about position 35, and said carboxy-terminal sequence consists essentially of about 120 to about 160 amino acid residues having an amino acid residue sequence of HBcAg from about position 10 about position 183, or

(b) said amino-terminal flanking sequence consists essentially of about 70 to about 90 residues having the amino acid residue sequence of HBcAg from about position 1 to about position 90, and said carboxy-terminal flanking sequence consists essentially of about 65 to about 85 amino acid residues having the amino acid residue sequence of HBcAg from about position 80 to about position 183.

23. The immunogen according to claim 25 wherein the number of amino acid residues present in said immunogenic polypeptide is about equal in number to the number of amino acid residues absent from said HBcAg amino acid residue sequence between the carboxy-terminal residue position of said amino-terminal flanking sequence and the amino-terminal residue of said carboxy-terminal flanking sequence.

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- 24. The immunogen according to claim 18 wherein said immunogenic polypeptide has a length of about 10 to about 30 amino acid residues.
- 25. An isolated and purified DNA molecule that encodes a cholesteryl ester transfer protein (CETP) immunogen that comprises (i) a DNA sequence that encodes an immunogenic polypeptide having a CETP amino acid residue sequence that is operatively linked to (ii) a DNA sequence that encodes an exogenous antigenic carrier.
  - 26. The isolated and purified DNA molecule according to claim 25 wherein said immunogenic polypeptide is encoded by a DNA of SEQ ID NOs:1, 27 or 31.
  - 27. The isolated and purified DNA molecule according to claim 26 wherein said exogenous antigenic carrier is encoded by a DNA of SEQ ID NO: 39 that encodes an amino acid residue sequence of SEQ ID NOs:40, 41, 42 or 43.
- 28. The isolated and purified DNA molecule
  25 according to claim 25 wherein the 3' end of the DNA
  encoding said exogenous antigenic carrier is operatively
  linked to the 5' end of the DNA encoding said
  immunogenic polypeptide.
- 29. The isolated and purified DNA molecule according to claim 25 wherein said first-named DNA (i) encodes an immunogenic polypeptide having a length of about 10 to about 30 amino acid residues.

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- 30. The isolated and purified DNA molecule according to claim 29 wherein said second-named DNA (ii) has two portions, one of which is operatively linked to the 5' and of said first-named DNA and another of which is operatively linked to the 3' end of said first-named DNA, wherein
- (a) said one portion encodes an aminoterminal flanking sequence that consists essentially of about 10 to about 20 amino acid residues having an amino acid residue sequence of the hepatitis B core protein (HBcAg) from amino acid residue position 1 to about position 35, and said other portion encodes a carboxyterminal flanking sequence that consists essentially of about 120 to about 160 amino acid residues having an amino acid residue sequence of HBcAg from about amino acid residue position 10 to about position 183, or
- (b) said one portion encodes an aminoterminal flanking sequence that consists essentially of about 70 to about 90 amino acid residues having the amino acid residue sequence of HBcAg from about amino acid residue position 1 to about position 90, and said other portion encodes a carboxy-terminal flanking sequence that consists essentially of about 65 to about 85 amino acid residues having an amino acid residue sequence of HBcAg from about amino acid residue position 80 to about position 183.
- 31. The isolated and purified DNA molecule according to claim 30 wherein said first-named DNA (i) encodes an immunogenic polypeptide of SEQ ID NOs:2-7, 8-13, 29, 32-37 or 50.
- 32. The isolated and purified DNA molecule according to claim 31 wherein said isolated DNA molecule consists essentially of a DNA segment that encodes amino

acid residues 1-69 of HBcAg (SEQ ID NO:38) operatively linked at its 3' end to the 5' end of DNA that encodes amino acid residues 461-476 of CETP (SEQ ID NO:29) whose 3' end is operatively linked to the 5' end of a DNA segment that encodes amino acid residues 76-183 of HBcAg

(SEQ ID NO:38).

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## Abstract of the Disclosure

A process for increasing the concentration of HDL cholesterol in the blood of a mammal whose blood contains cholesterol ester transfer protein (CETP) is contemplated. That process comprises the steps of: (a) immunizing the mammal with an inoculum containing a CETP immunogen that is an immunogenic polypeptide having a CETP amino acid residue sequence that is covalently bonded to an exogenous antigenic carrier polypeptide and is dissolved or dispersed in a vehicle; and (b) maintaining the immunized mammal for a time period sufficient for said immunogenic polypeptide to induce the production of antibodies that bind to CETP and lessen the transfer of cholesteryl esters from HDL. Immunogens, inocula and DNA segments useful for carrying out the invention are also disclosed.

6018/6,9242

## DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare:

That my residence, post office address and citizenship are as stated below next to my name.

That I verily believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural inventors are named below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

AN IMMUNOLOGICAL PROCESS AND CONSTRUCTS FOR INCREASING THE HDL CHOLESTEROL CONCENTRATION

the sp	ecification of which (check one)					
	is attached hereto.					
X	was filed on	as as				
hv ar	That I have reviewed and understand the cory amendment referred to above.	ntents of the above	-identified specification, in	ncluding the clai	ms, as amended	1
D accor	That I acknowledge the duty to disclose dance with Title 37, Code of Federal Regularity That I hereby claim foreign priority benefit or inventor's certificate listed below and ficate on this invention having a filing date	lations, §1.56(a).  ts under Title 35, have also identifie	United States Code, §119 of the below any foreign apple	of any foreign apication for pater	oplication(s) fo	r
				Priority	Claimed	
	Foreign Application(s)				. 🗆	
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(Nur	nber) (Country)		(Day/Month/Year Filed	) 		
				Yes	No	
(Nu	nber) (Country)		(Day/Month/Year Filed	)		
in the	That I hereby claim the benefit under Title insofar as the subject matter of each of the one manner provided by the first paragraph erial information as defined in Title 37, Cooperior application and the national or PCT in tend States. Application(s)	claims of this applied of Title 35, United to Federal Reguleration	cation is not disclosed in the distates Code, §112, I acations, §1.56(a) which occurred	knowledge the	duty to disclo	se
Onn	ted States Application(s)					
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That all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

I hereby appoint the following attorneys, with full power of substitution and revocation, to prosecute this application and to transact all business in the United States Patent and Trademark Office connected therewith and request that all correspondence and telephone calls in respect to this application be directed to WELSH & KATZ, LTD., 120 South Riverside Plaza, 22nd Floor, Chicago, Illinois 60606, Telephone No. (312) 655-1500:

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joint inventor, if any:					
Inventor's signature:	Elaine S. Rul				
Date:	February 13, 1997				
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	Warson Woods, MO 63122-1636				
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Citizenship:	- CANADA				
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Inventor's signature:	Soud P. Land				
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